

FIG.1

HPP-CFC (Colony #)

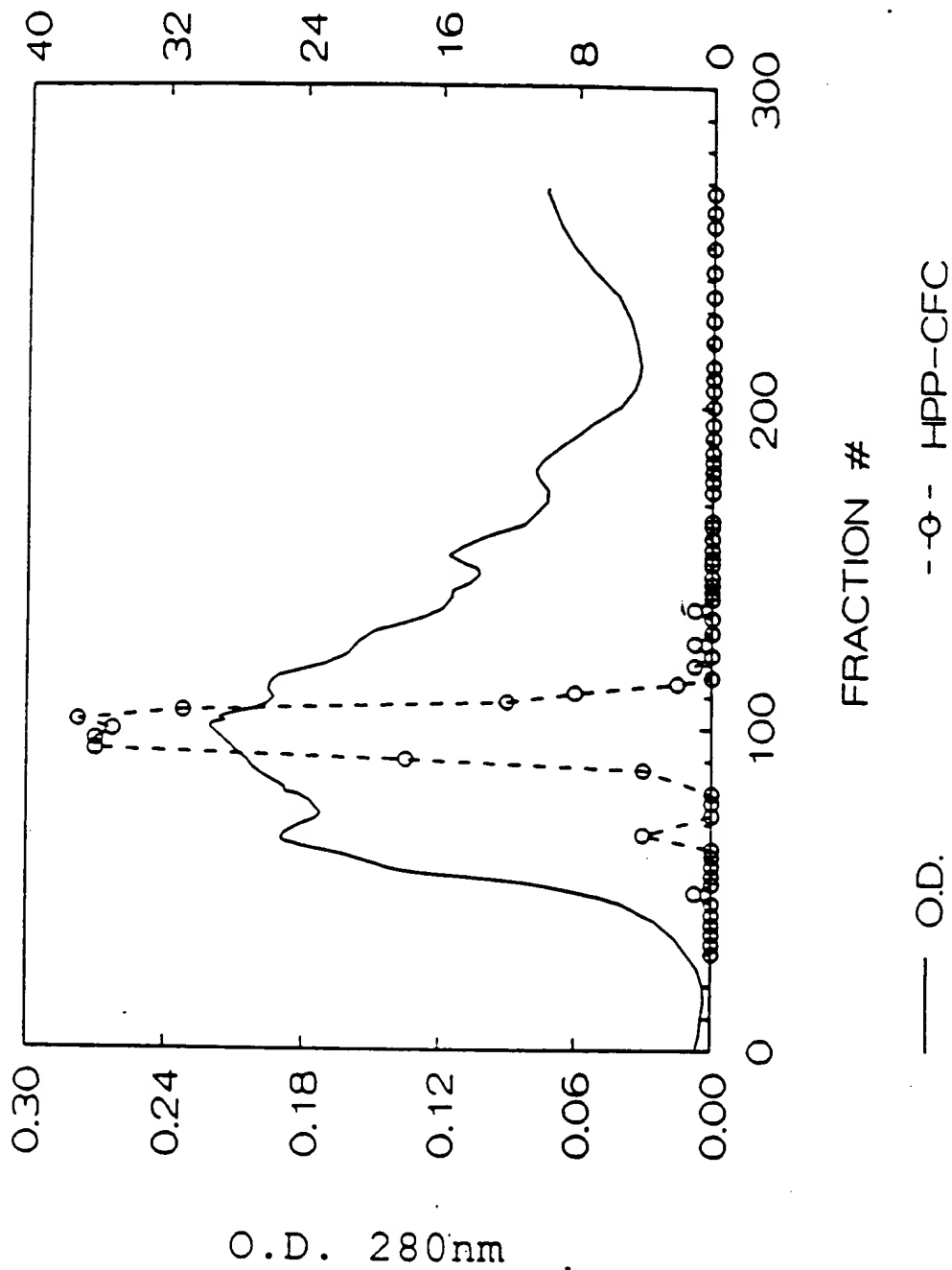


FIG.2

HPP-CFC (Colony #)

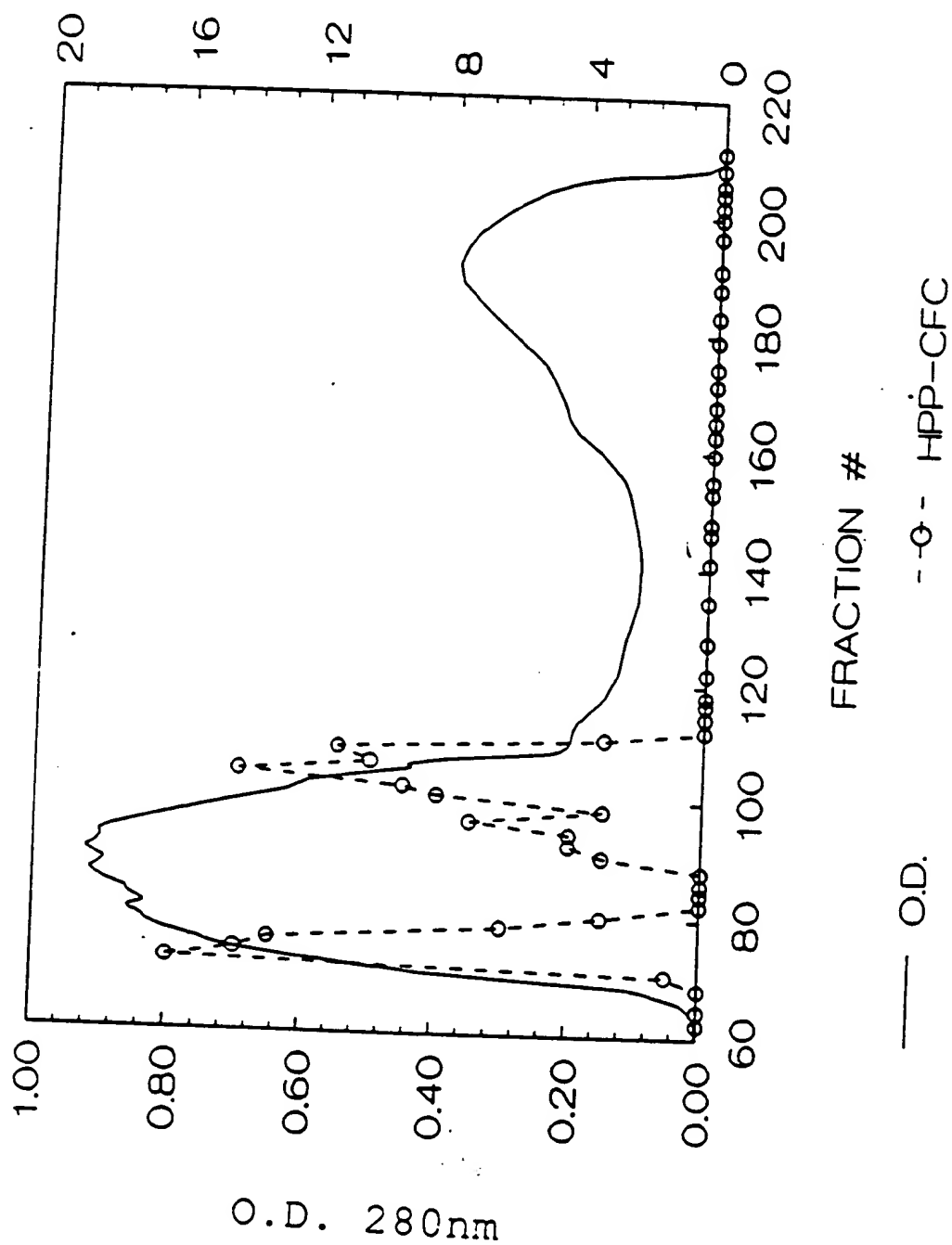


FIG.3

MC/9 CPM ($\times 10^{-3}$) OR HPP-CFC (COL. #)

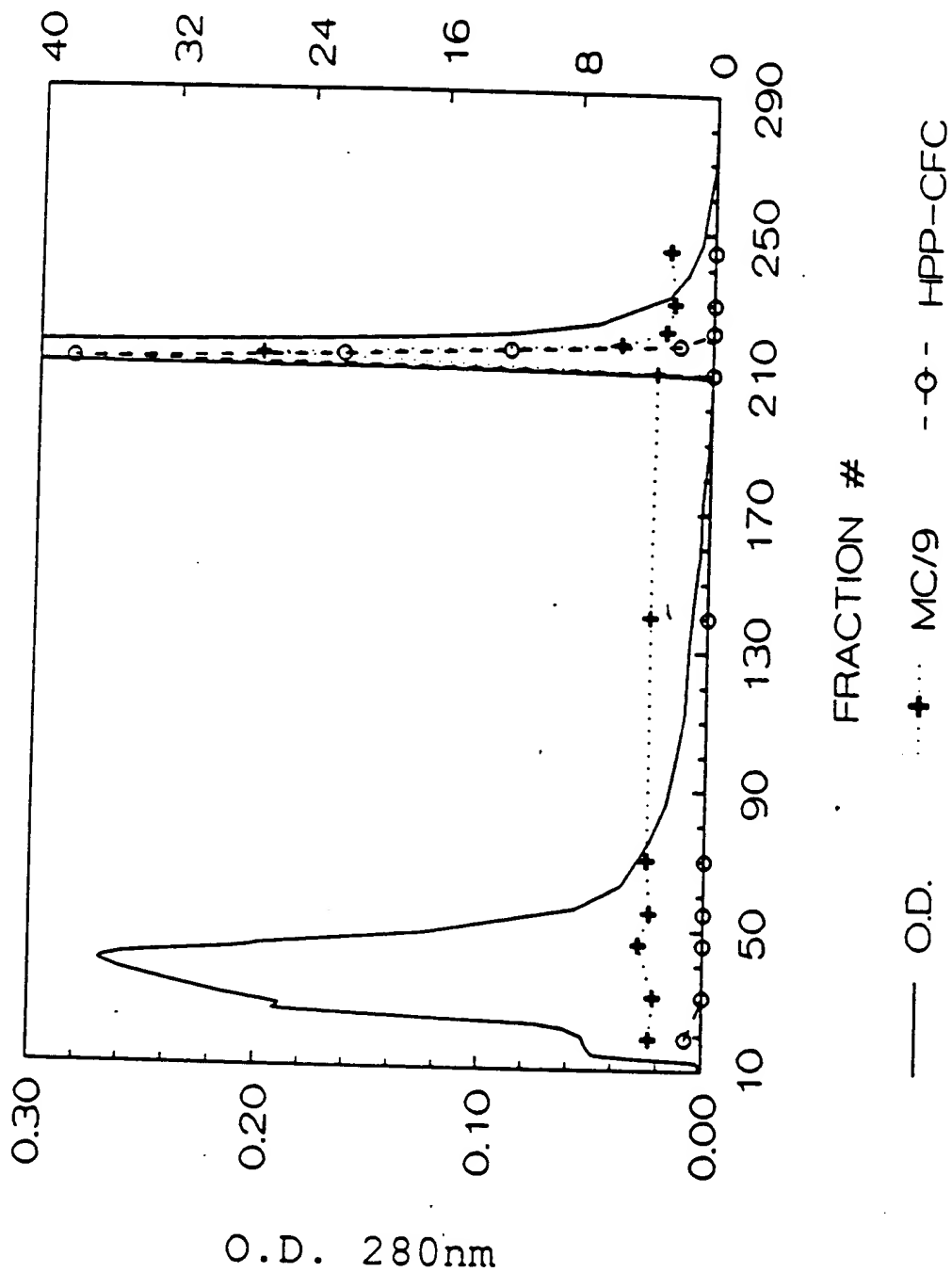


FIG. 4

MC/9 CPM ($\times 10^{-3}$)

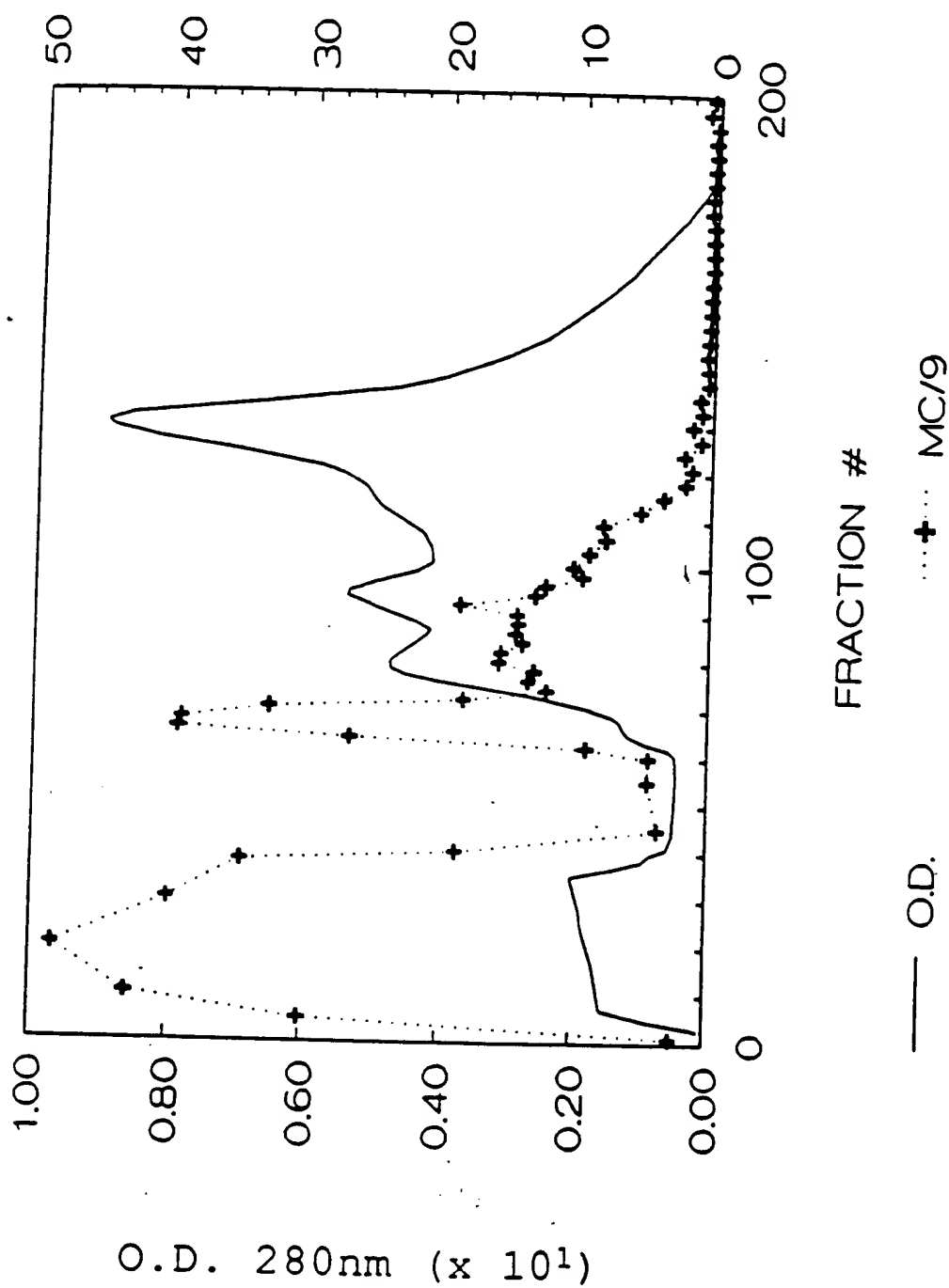


FIG.5

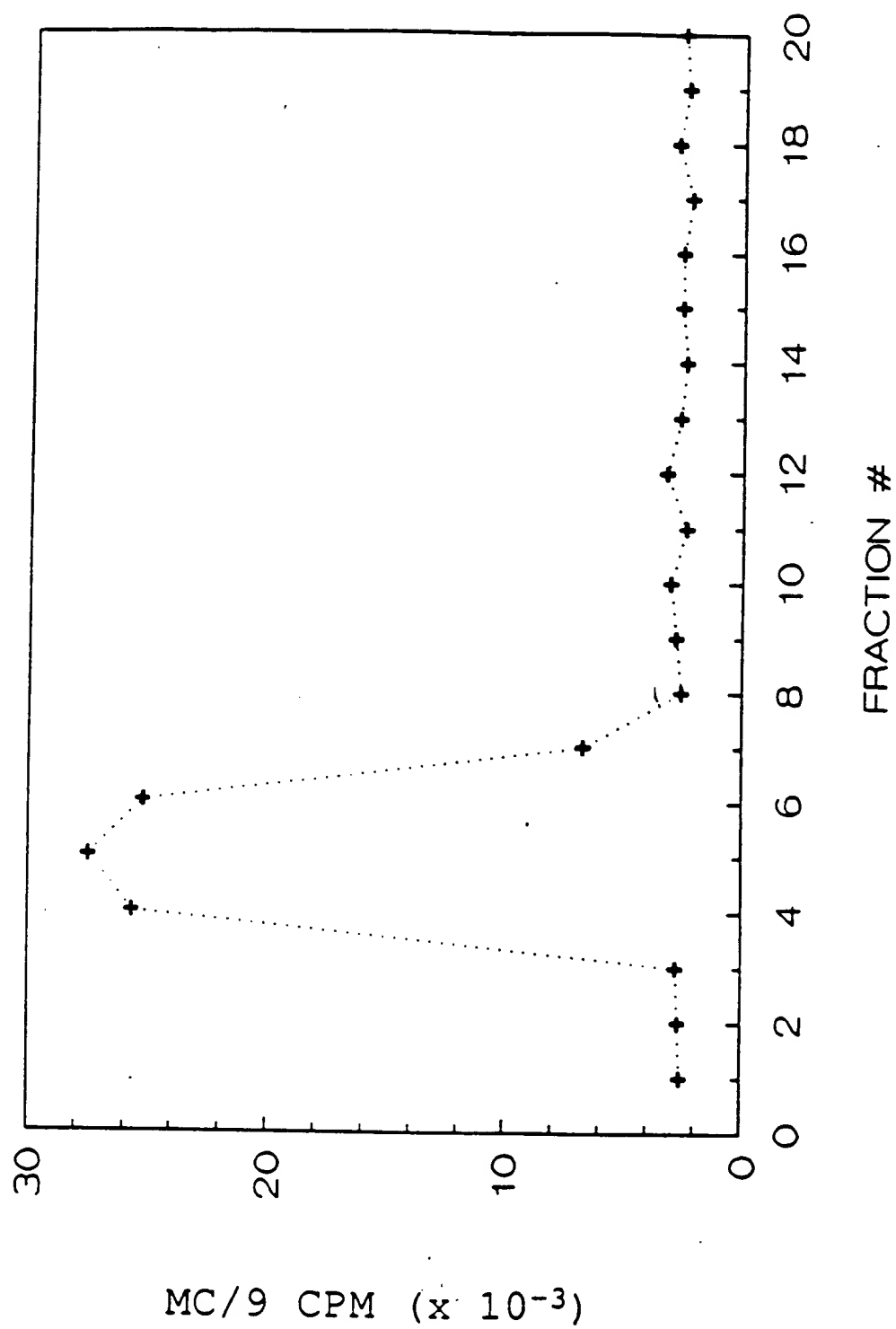


FIG. 6

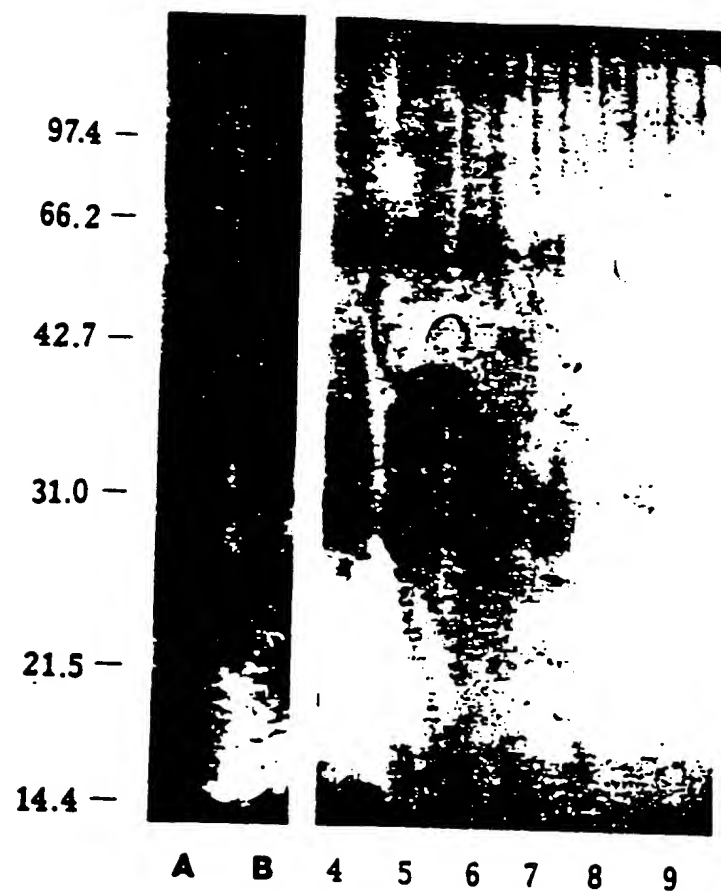


FIG.7

MC/9 CPM

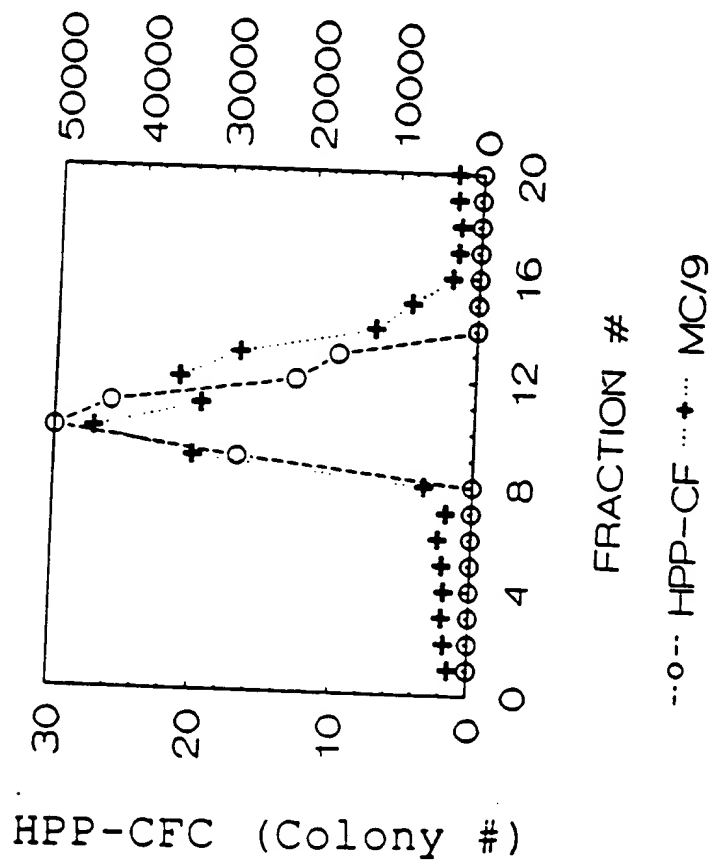


FIG. 8

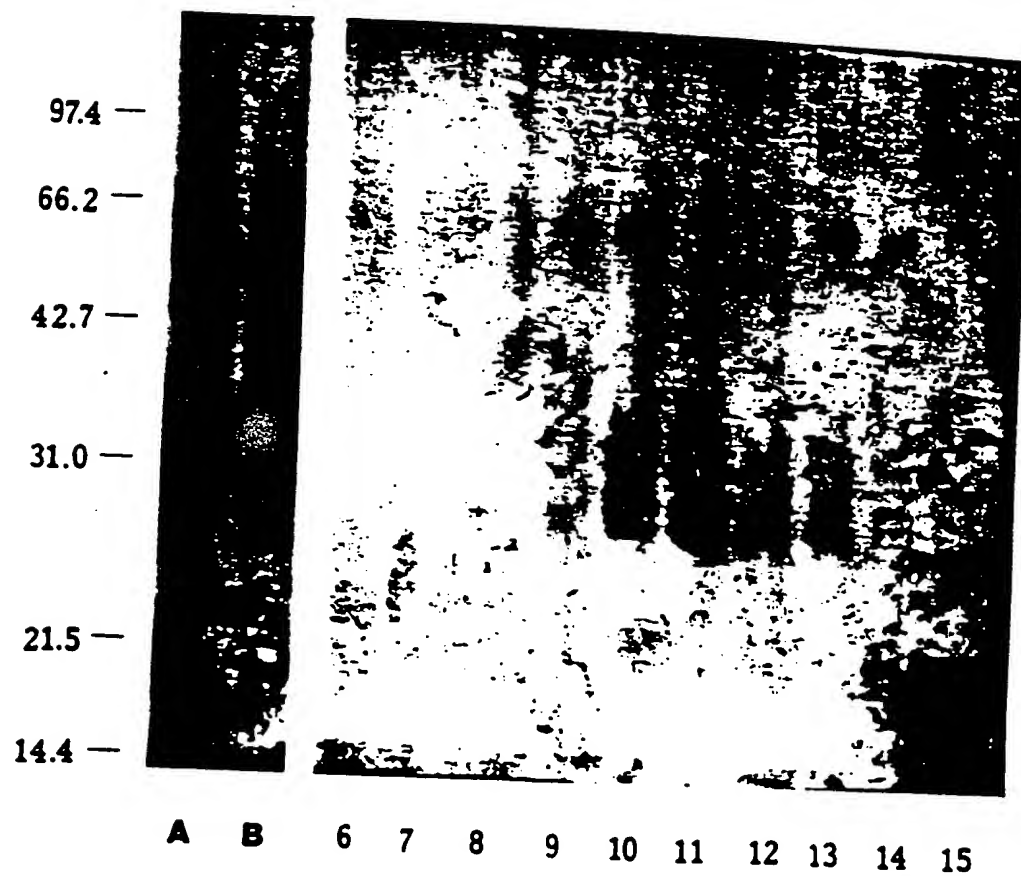


FIG.9

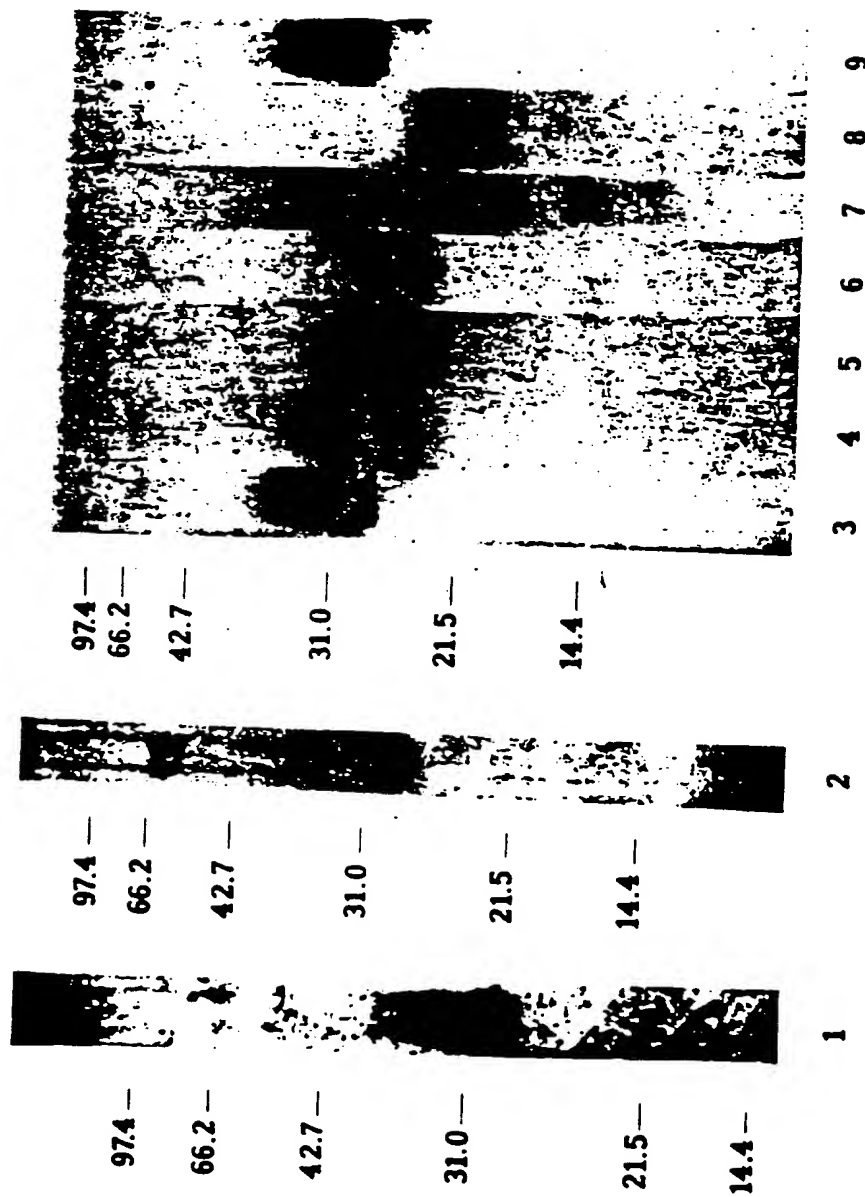


FIG.10

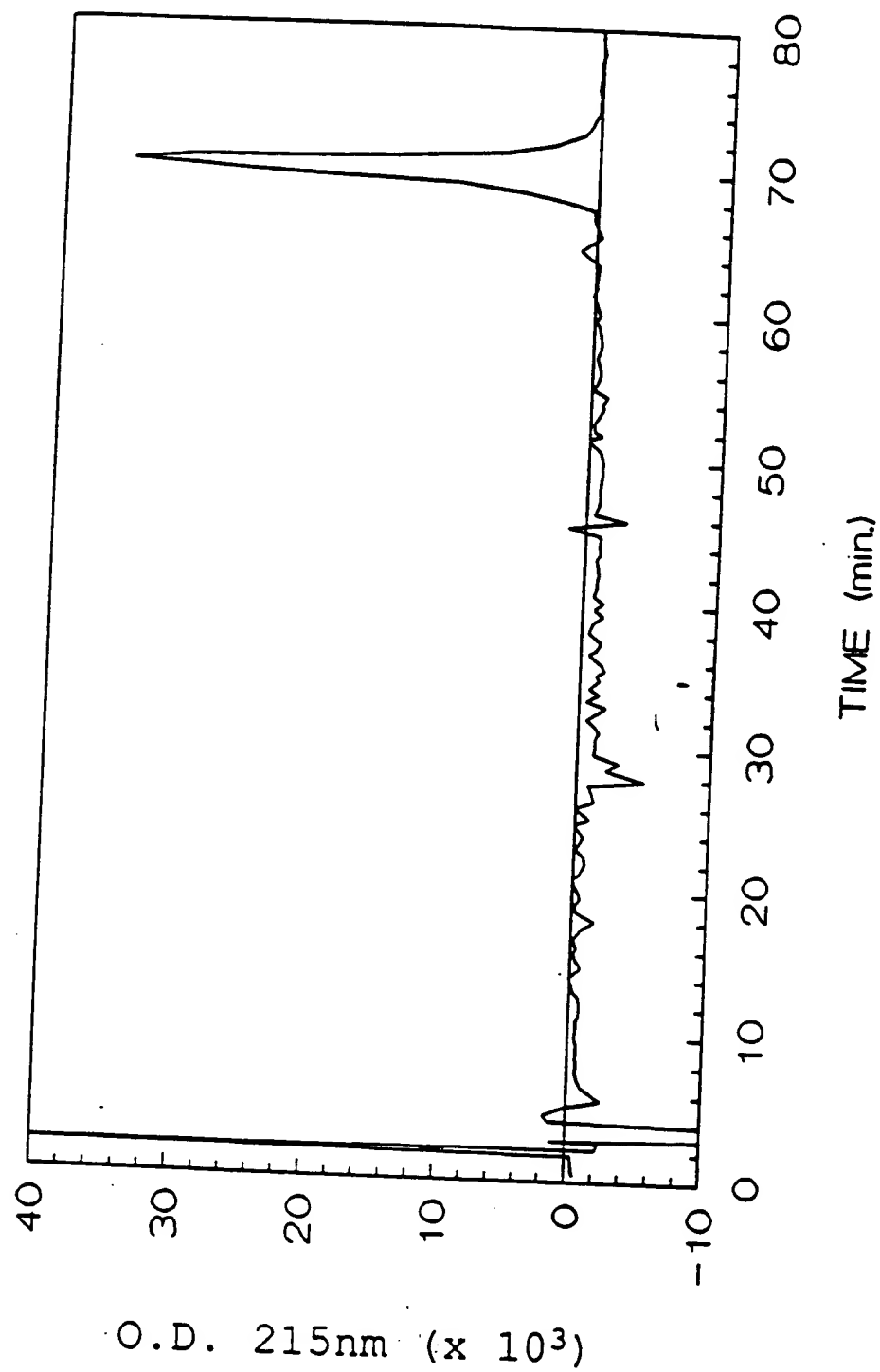


FIG. 11

1 10 20
 pE E I C R N P V T D N V K D I T K L V A N L P N D
 ----- Sequencing after
 ----- T-5a -----
 30 40 50
 Y M I T L N Y V A G M D V L P S H C W L R D M V T
 <Glu Aminopeptidase Treatment ----->
 ----- T-5a -----
 ----- CB-6a ----- CB-8; CB-10 -----
 60 70
 H L S V S L T T L L D K F S **N** I S E G L S **N** Y S I
 ----- Sequencing after Trp Cleavage -----
 80 90 100
 I D K L G K I V D D L V A C M E E N A P K N V K E
 ----->
 ----- T-3 -----
 ----- CB-14; CB-15; CB-16 -----
 ----- S-1 -----
 110 120
 S L K K P E T R **N** F T P E E F F S I F **N** R S I D A
 --- T-1 ----- T-4 (N109 nonglyco) -----
 --- T-7 (N120 glyco); T-8 (N109 nonglyco) -----
 ----- CB-14; CB-15; CB-16 -----
 ----- S-5 or S-6 (N109 nonglyco) -----
 130 140 150
 F K D F M V A S D T S D C V L S **S** **T** L G P E K D S
 ----- T-5b -----
 ----- CB-6B -----
 ----- S-5 or S-6 -----
 160
 R V S V **T** K P F M L P P V A(A)
 --- T-2 ---
 ----- CB-6B -----
 ----- S-2 -----
 <--- (Carboxypeptidase)

FIG.12A

OLIGO	SEQUENCE	LOCATION
219-21	ACATTCTTTIGGIGCATTTCTCCTCCAT G T G T T	393-368
219-22	AAAACTCCTCIGGIGTAAATTT G T T G G	447-425
219-25	GTTCNGGTTTTTT C C C	420-407
219-26	ATGGAAGAAACGCCCCCAAAACGT G G T G T	368-393
222-11	CCNAATGATTATGATAAC C C C C T	167-186
222-12	GGNGGNAACATAAANGGCTT G G T	566-585
223-6	ACCATAAAATCTTTAAACGATC G G C G G	492-470
224-24	GTATTTTCAATAGATCCATTGA	450-471
224-25	CCAACTATGTCGCC	190-202
224-27	GTAGTCAAGCTGACTGATAAG	273-253

FIG.12A CONT.

224-28	TAACCAACAATGACTAGGCAA	235-215
225-31	TTCCAGAGTCAGTGTC	547-562
227-29	GCGAAGCTTGCCTTTCCTTATGAAGAAGA	16-35 *
227-30	GCGCCGCGGTTACGGTGGTAAACATGAAGGCTTTGTGA	586-561 *
228-30	GATAAATGCAAGTGATAATCC	45-65
230-25	GCGGTCGACCCGCGGAACCTTAAAGTCCATGCAACAC	705-685 *
237-19	CACCCGCGGTTATGCAACACAGGGGGTAACATAAATGG	569-592 *
237-20	CACCCGCGGTTAGGCTGCAACACAGGGGGTAACATAAA	572-595 *

FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCACCTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190 *

FIG.12C

OLIGO	SEQUENCE
201-7	CCCCCCCCGG T A
220-3	TTTTTTTTTTTTTTTTTTGG
220-7	TTTTTTTTTTTTTTTTTTAG
220-11	TTTTTTTTTTTTTTTTTTTCG
221-11	TTCGGCCGATCAGGCCCCCCCCC
221-12	TTCGGCCGATAGGCCTTTTTTTTTTTTTT
228-28	GGCCGGATAGGCCTCACNNNNNT
228-29	GGCCGGATAGGCCTCAC

FIG.13A

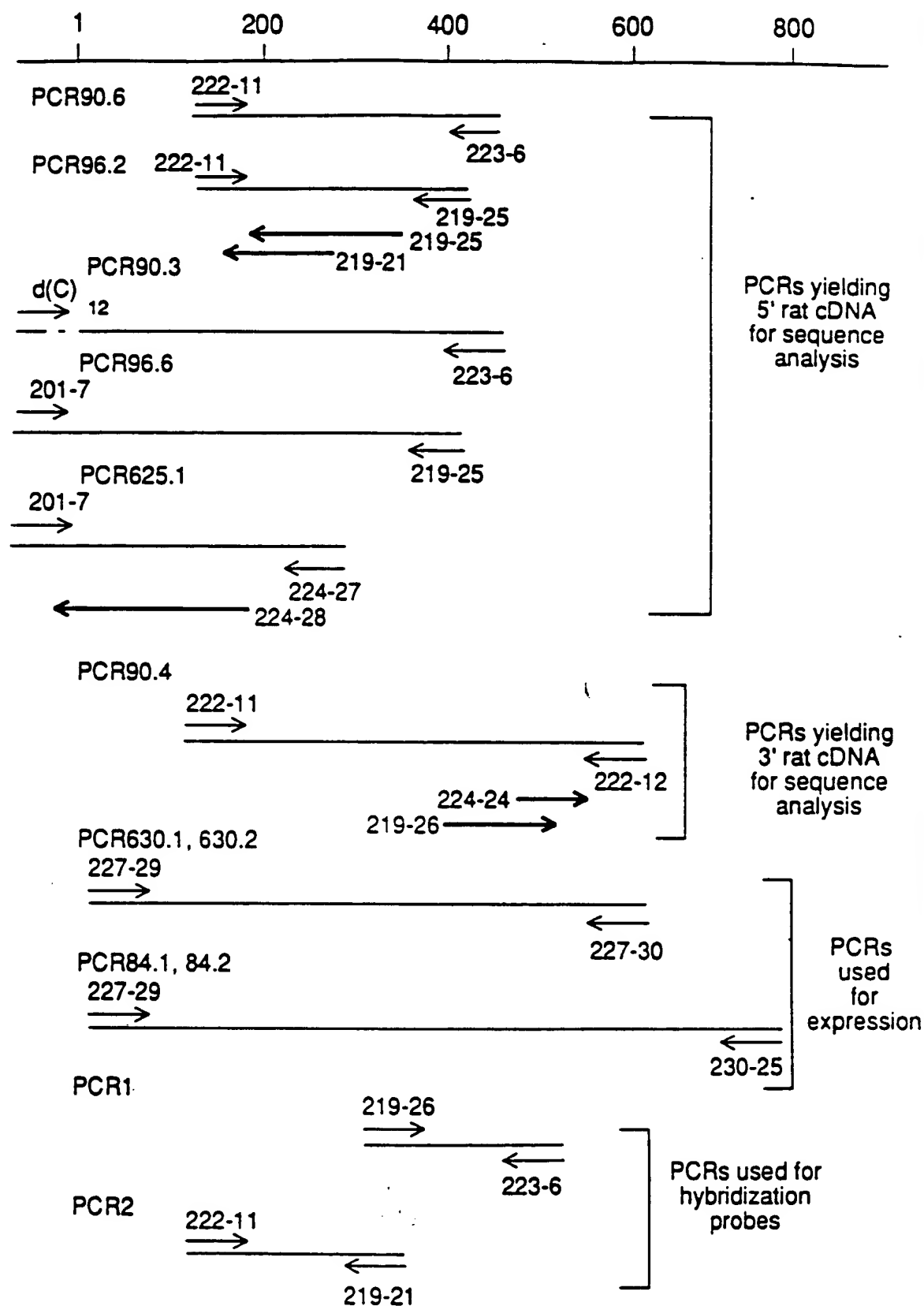


FIG. 13B

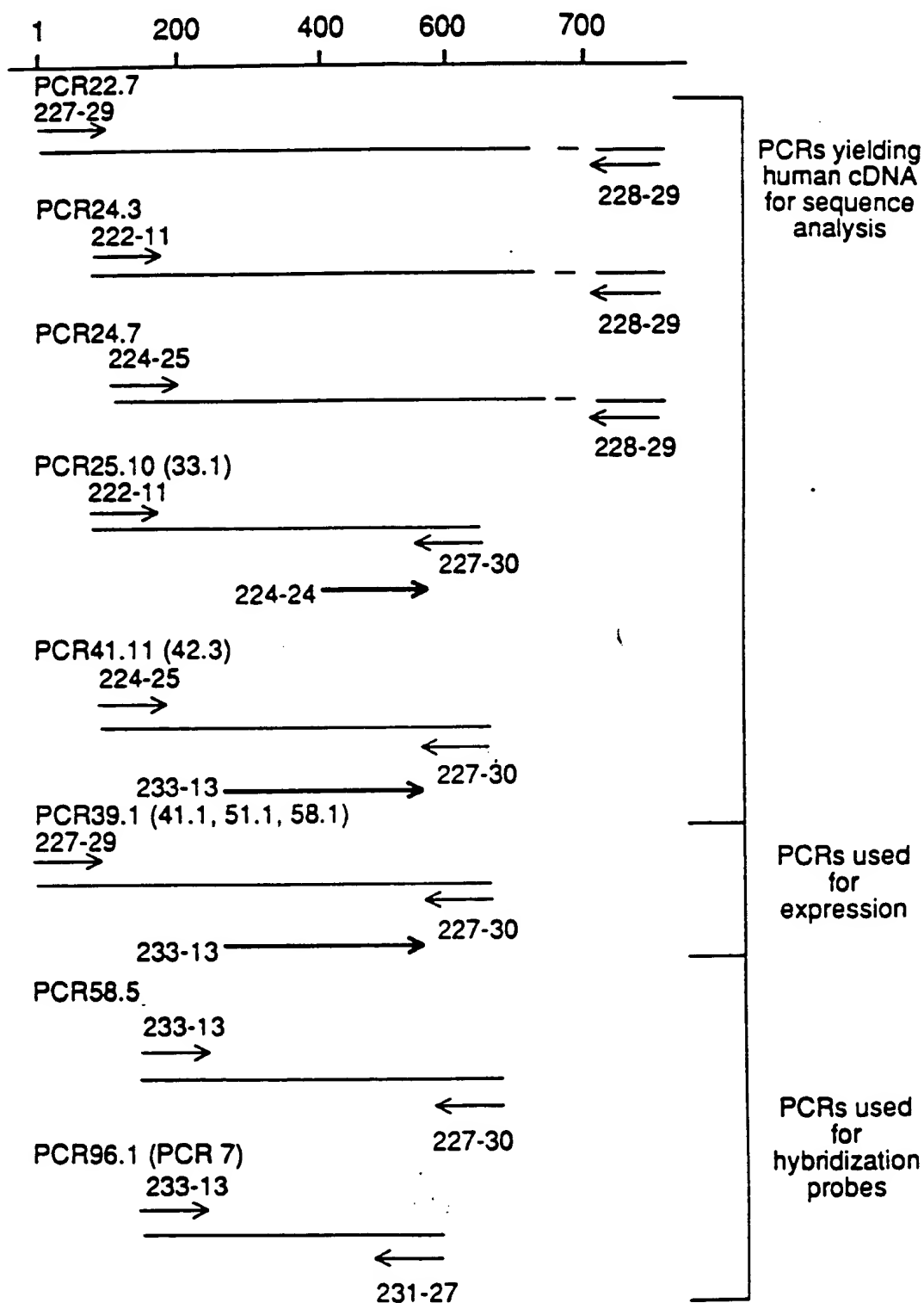


FIG.14A

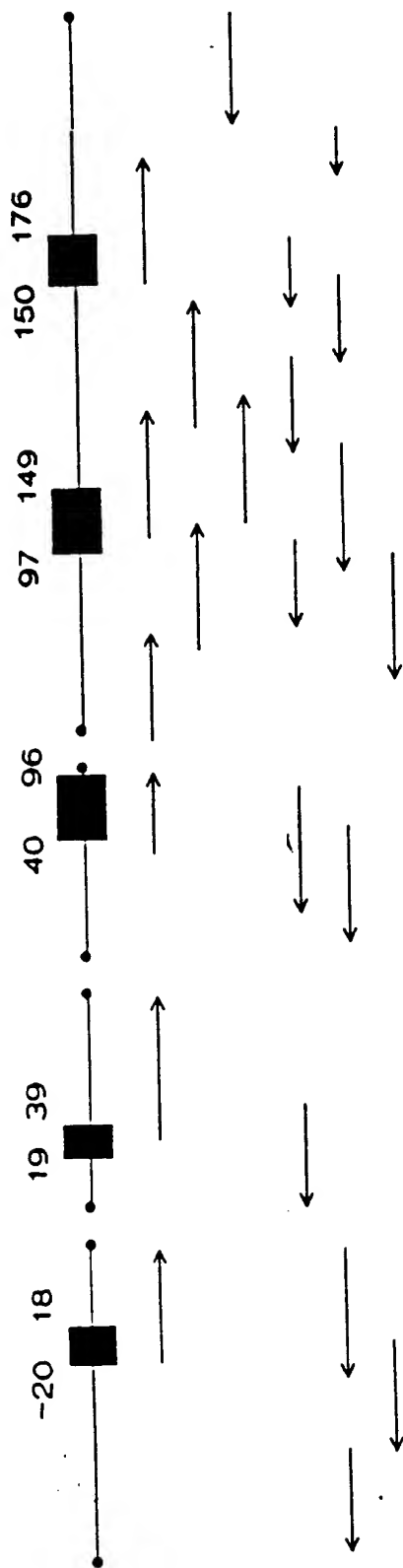


FIG.14B

AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCcATAAGTGGT 45
 AAACAnACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT 90
 TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA 135
 TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT 180
 TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAAGG 225
 AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTTTCATGCATTCCT 270
 CCATTTTCCGAGGTCCCCccCcAAGTGATAATTCTGTTACACGTTG 315
 CTACAAGTTCATCCCTAATTGCCGTCAAGAACTGACTGTAGAAG 360
 GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT 405
 AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC 450
 TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT 495
 AAGCCATCAGCTTAAAACAAAACAAAACAAAACAAAACAAAACCC 540
 CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC 585
 TGGTTTGCATAGTTCTGGATTTTTTTTTTTTTTAAAACTGATGGAC 630

-20

ThrTrpIleIleThrC
 ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT 675

-10

ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG
 GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTC 720

1

10

lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT
 AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA 765

18

hrLysLeu

FIG.14B CONT.'

CAAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC	810
CTGTGCTTGCTGACCACATAGGTTTCAGGGCACTCCCGACAGGAGT	855
TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC	900
TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC	945
TGTATAACTGGCCCTTTGCACACCAACAAAGTGACTGACTGGCTT	990
TTGCCTGTTACCTACTG	1007

Intervening sequence of unknown length

TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA	45
TTTACAACTCAAGCATTATATATTGGACAACnACGGGGTATGAGA	90
TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT	135

19

Val

TCTCTTGTATTTACTCACGTTTTTCATTTCTTGGTCTCTGTAGGTG	180
--	-----

30

AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla	
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC	225

39

GlyMetAspValLeu

GGGATGGATGTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT	270
---	-----

TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT	315
---	-----

TATTTGCTCTTTGTCGTTTTTAGATGTTGACCTATAATTTTTCCT	360
---	-----

TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT	405
---	-----

TAAGCCTACTCATTAAAAGGAAATGGCTCATCTTAGACGTAGCAA	450
---	-----

FIG.14B CONT.'

CCGATGTTAATTTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG	495
TTAAAATCATGTTAAATTTCTCCTTGGCTATGTTATTTCTCATG	540
GCTATGTTATTCCTATTCGTATTTTCAATTTAAAGGGACGGAATATT	585
TATTGTATTTCTGAACTTTTTTCAGGCATGCATCCGGGTCTTTGAA	630
TAAAA	635

Intervening sequence of unknown length

CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA	45
ATGTCTTTGAAAACGCAGTGACTAAGCCATAAATAATCTTCCACA	90
GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGGTGGGGCAAG	135
AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG	180
GGTGGTTTAAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT	225
TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT	270
TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAACTCTTTGTCTCT	315
GCAGTCAGTGACTAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA	360
ATCTGCCATATTTTTTAATAGATGCTTTGTCTTCTCTTTGAATTTT	405

40.

50

ProSerHisCysTrpLeuArgAspMetValThrHisLeu	
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA	450

60

SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer	
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT	495

70

80

GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle	
---	--

FIG.14B CONT.'

GAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATA 540

90 96
ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA 585

ACTTGGTATTCATCAGAATTATTTTCTTATACT 619

Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA 45

GAGGACATTATCCCCTCTTTGGATGCCATAGGAATCTGCTCTCAA 90

ATATGTAGATAACCACTCTGCCACCTCAGCACATACATACACATA 135

ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC 180

TTTTCTGTATTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT 225

TTAAAGGCTAATTCTTATTTTGTAAATAAGCAGCTTTAAATTTCTT 270

AATTGTTTTTTTCGGGTCACCTTTATTGTCCTATTGCCACGACATTG 315

TCCTGTCCCATTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC 360

CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC 405

TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTAAATT 450

ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC 495

AGTCAAGTCTATGAGTTATTTGAAAACCTAGAATCTTTGTTAATTA 540

97
AsnValLys
TTTGTGTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA 585

100 110
GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu

FIG.14B CONT.'

GAATCACTGAAGAAGCCAGAACTAGAACTTTACTCCTGAAGAA	630
120	
PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC	675
130	140
MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA	720
148	
GlyProGluLysA GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTCTTGTTTAAATGT	765
ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC	810
TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA	855
ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT	900
GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA	945
AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT	990
GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA	1035
AGATTTACAGTCTCATGTCTTTTCCATAAGGTTCAAACCTCTGAGA	1080
CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC	1125
CCGAGCTGGGTCCCTATGGGGGAACATACTTCATTGCTTTCTTTT	1170
AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT	1215
TCCTAAGCATGTCTGTGCATGCATAAGCCTTCACTCTACAAGAC	1260
AGTTATGGTGTATCGCTTGACAAAACCTGAGCAGCCAAGCTGAGTA	1305
TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT	1350
GATATTGCACTTCGCCTTTGGGGGACTCTATGATTCAAAAGTTCA	1395

FIG.14B CONT.

	150	
	spSerArgV	
CCATGTAACACTGACACATTATTGCTTTCTATTTAGATTCCAGAG		1440
	160	
alSerValThrLysProPheMetLeuProProValAlaAlaSerS		
TCAGTGTACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGTT		1485
	170	176
erLeuArgAsnAspSerSerSerSerAsn		
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC		1530
TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT		1575
GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG		1620
TCACTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG		1665
TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA		1710
ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTTAAATAAGGCAC		1755
GAAATTAATTGAAGGAAAAAAAAAATACAAGCAAGGCCTTATTTTG		1800
AATCATGGTAGGCTTAAATAGACTTTGTGGAGAATGTCCCTGAT		1845
CAAAGTGGAGTTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC		1890
AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG		1935
CATGTTTGGAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA		1980
TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT		2025
TGcCCAAGAACCCAcGTTCCCTGGAAGACTATCTTATTTTCATGTC		2070
TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT		2115
CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA		2160
AAGAAAGTTCTCTGAAGTCCATGCTTTAGAATGTTTCTCTATCAA		2205

FIG.14B CONT.'

AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC	2250
CCTGAAAAATATATTTACAGTGTAGACATTTGATATACATCTAA	2295
GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC	2340
CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC	2385
ATGCATATAACATATCAGATCCTCGAGC	2413

FIG.14C

```

-25          -20
M K K T Q T W I I T C I
CTGGATCGCAGCGCTTCCTTATGAAGAAGACACAAACTTGGATTATCACTTGCAT 60

-10          1
Y L Q L L L F N P L V K T Q E I C R N P
TTATCTTCAACTGCTCCTATTAACTCTCGTCAAAACTCAGGAGATCTGCAGGAATCC 120

10          20
V T D N V K D I T K L V A N L P N D Y M
TGTGACTGATAATGTAAAGACATTACAAAACCTGGTGGCGAATCTTCCAAATGACTATAT 180

30          40
I T L N Y V A G M D V L P S H C W L R D
GATAACCCCTCAACTATGTGCGCGGGATGGATGTTTGGCCTAGTCATTGTTGGTTACGAGA 240

50          60
M V T H L S V S L T T L L D K F S N I S
TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTC 300

70          80
E G L S N Y S I I D K L G K I V D D L V
TGAAGGCTTGAGTAATTATTCATCATAGACAAACTTGGGAAAATAGTGGATGACCTCGT 360

90          100
A C M E E N A P K N V K E S L K K P E T
GGCATGTATGGAAGAAATGCACCTAAGAATGTAAAGAATCACTGAAGAAGCCAGAAAC 420

110          120
R N F T P E E F S I F N R S I D A F K
TAGAACTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTGATGCCCTTCAA 480

```

FIG.14C CONT'

130 D F M V A S D T S D C V L S S T L G P E
 GGACTTCATGGTGGCATCTGACACTAGTAGTGCTCTCTTCAACATTAGGTCCTGA 540
 140
 150 K D S R V S V T K P F M L P P V A A S S
 GAAAGATTCAGAGTCAGTGTACAAAACCATTTATGTTACCCCTGTTGCAGCCAGTTC 600
 160
 170 L R N D S S S S N R K A A K S P E D P G
 CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAAGCCGCAAGTCCCCCTGAAGACCCAGG 660
 180
 190 L Q W T A M A L P A L I S L V I G F A F
 CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTGCTTGAATGGCTTTGCTTT 720
 200
 210 G A L Y W K K K Q S S L T R A V E N I Q
 TGGAGCCTTATACTGGAAGAAGAAACAGTCAAGTCTTACAAGGGCAGTTGAAAATATACA 780
 220
 230 I N E E D N E I S M L Q Q K E R E F Q E
 GATTAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGTTTCAAGA 840
 248
 V
 GGTGTAATT 849

FIG.15A

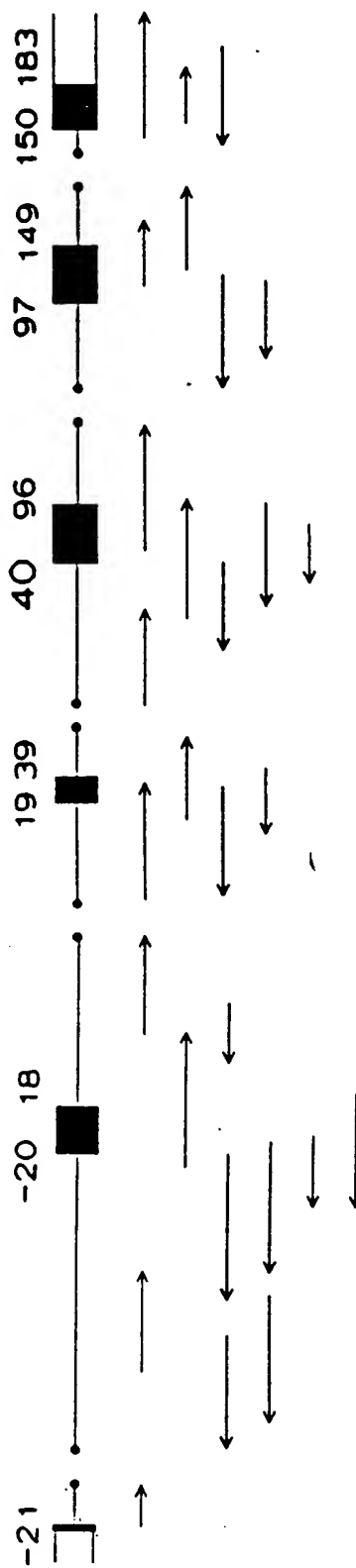


FIG.15B

-21
hrGln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA	45
AAAATCGCGCCCGGTGCCCCGGGGaAGCCGGCGCTCCCTGGGACT	90
TGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTG	126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA	45
CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT	90
ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG	135
TGTTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT	180
TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG	225
GCTAAAAAGCTGTGTTTCAAATATTCTTTTGATGTCTCACAAAT	270
TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT	315
TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA	360
GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA	405
ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT	450
CTCTAGTTTTTTAGAAGATACCCTAAGGGCTAAGTCTTTAACATGC	495
TGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA	540
AAGTTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT	585
CAAAATGGATTTTAACTAAAAGCTTTTAAAACTTTGGTGAGCAT	630
AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT	675

FIG.15B CONT.'

ATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT	720
TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTC	765
<div>-20</div> <div>ThrTrpIleLeuThrCysIleTyrLeuGlnLe</div> <div>-10</div>	
TGTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT	810
<div>1</div> <div>uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs</div> <div>GCTCCTATTTAATCCTCTCGTCAAACTGAAGGGATCTGCAGGAA</div>	855
<div>10</div> <div>nArgValThrAsnAsnValLysAspValThrLysLeu</div> <div>18</div>	
TCGTGTGACTAATAATGTAAAAGACGTCCTAAATTGGTAAGTAA	900
GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTT	945
CCTGTGCTTGTTGATAAAAGATTTAGATTTTTCTTGCCCCAAAGT	990
AATGTTTTCTTAAAGTGGGGAAAGTAATCACTGGGTTACAATAAA	1035
GGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA	1080
TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCT	1125
TCTTTGCTGGTCTTCTCCCCATCCTTCATAGGCAGTGAAGGACCT	1170
TGGAGAGTTCGCTGTGTGCTGATGGGCTTGCCCCAGCTTGTTCCC	1215
CATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA	1260
CATGTCTTCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCT	1305
GAAATGGCTATTCTCCCAATTCAATCAGCAGGAAGACCCTGTCAC	1350
ATGTCAGTGGGTGTTTGCTCCTTCAGGGAACATAGAGAGGTGATT	1395
CATTGCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT	1440
TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC	1479

FIG.15B CONT.'

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC	45
CAAACTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA	90
GTCTAAAAGATCTGTATTATCACTTTTTTATTTTGAAGGATGCCT	135
TTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT	180
AAATATTGAAATTCATTGGTAACTTTAAAAAGCACACAGTTTTG	225
TGTGCTTTTCTCCAAAGCACTACAAATATGATTAATTGATGTATA	270
19	
ValAlaA	
AGAATTTTCTTATGGAATTTTTTTTTTTGTCTCTGTAGGTGGCAA	315
30	
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM	
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA	360
39	
etAspValLeu	
TGGATGTTTTGGTATGTAACTACATTTCTGAGTTTCATTTTAGT	405
AGCTCATAGAAGAAATGGGATCATTATGAGATAGTACACTA	450
GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA	495
TCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT	535

Intervening sequence of unknown length

CCTGTTACAAGAGTCCCTCCTCCTATTAGAATAGTCCCTCCTCCT	45
CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC	90

FIG.15B CONT.'

CTCCTATTACAACATTTTAAGTAATGTAATATTAATTTTAAAAAT	135
CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG	180
AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAG	225
CCTGGCCAACATGGTGAACTTCCTCTCTACTAAAAATAAAAAAG	270
TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA	315
GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG	360
AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAATAAGCTGT	405
40	
ProSerHisCysTrpIleS	
TTTGTCTCTTTTTTCATATCTTGCAGCCAAGTCATTGTTGGATAA	450
50	
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA	60
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG	495
70	
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI	
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA	540
80	
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL	90
TAGACAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGA	585
96	
ysGluAsnSerSerLys	
AAGAAAACATCTAAGGTAACCTTGTGTTTCATTGGGATTATTTT	630
TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG	675
AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC	720
AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTG	765
CAGTTATACTGCAATACTGAAGTGCACATTC	796

FIG.15B CONT.'

Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA	45
CTACCCTGCATTACCAATCTGAATTACATACGTAAACAGCCAT	90
CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA	135
GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA	180
97	
CTATTTGAAAAATGTAATCCTATTTTTTTCTTCTAGGATCTAAAAA	225
110	
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP	
AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT	270
120	
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV	130
TCTTTAGAATTTTAAATAGATCCATTGATGCCTTCAAGGACTTTG	315
140	
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS	
TAGTGGCATCTGAACTAGTGATTGTGTGGTTTCTTCAACATTAA	360
148	
erProGluLysA	
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTA	405
AACAACAAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG	450
TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG	495
CAGATATCAATAGCACAGAAGAAA	519

Intervening sequence of unknown length

FIG.15B CONT.'

CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG	45
<div style="display: flex; justify-content: space-between; margin: 0;"> 150 160 </div> <div style="display: flex; justify-content: space-between; margin: 0;"> spSerArgValSerValThrLysProPheMetL </div>	
CTTTCTATTTAGATTCCAGAGTCAGTGTCAAAAACCATTTATGT	90
<div style="display: flex; justify-content: space-between; margin: 0;"> 170 </div>	
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS	
TACCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA	135
<div style="display: flex; justify-content: space-between; margin: 0;"> 176 </div>	
erAsnA	
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA	180
ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAACTTCT	225
ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA	270
TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG	315
CTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTT	352

FIG.15C

-25

-20

M K K T Q T W I L T C I Y L Q
AAGCTTGCCCTTTCCTTATGAAGAAGACACAAACTTGGATTCTCACTTGCACTTATCTTCAG 61

-10

L L L F N P L V K T E G I C R N R V T N
CTGCTCCTATTTAATCCTCTCGTCAAAACTGAAGGGATCTGCAGGAATCGTGTGACTAAT 121

20

N V K D V T K L V A N L P K D Y M I T L
AATGTAAAGACGTCACCTAAATTGGTGGCAATCTTCCAAAAGACTACATGATAACCCCTC 181

40

K Y V P G M D V L P S H C W I S E M V V
AAATATGTCCCCGGGATGGATGTTTTTGCCCAAGTCATTTGTGGATAAGCGAGATGGTAGTA 241

60

Q L S D S L T D L L D K F S N I S E G L
CAATTGTCAGACAGCTTGACTGATCTTCTGGACAAGTTTCAAAATATTCTGAAGGCTTG 301

80

S N Y S I I D K L V N I V D D L V E C V
AGTAATTATTCATCATAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCCTG 361

100

K E N S S K D L K K S F K S P E P R L F
AAAGAAAACATCTAAGGATCTAAAAAATCATTCAGAGCCCCAGAACCCAGGCTCTTT 421

FIG.15C cont.

T P E E F F R I F N R S I D A F K D F V 130
 ACTCCTGAAGAATTCTTTAGAATTTTAAATAGATCCATTGATGCCCTTCAAGGACTTTGTA 481

V A S E T S D C V V S S T L S P E K D S 150
 GTGGCATCTGAAACTAGTGATGTGTGGTTTCTTCAACATTAAGTCCCTGAGAAAGATTCC 541

R V S V T K P F M L P P V A A S S L R N 170
 AGAGTCAGTGTCAACAAACCATTATGTACCCCTGTGTCAGCCAGCTCCCTTAGGAAT 601

D S S S N S K Y I Y L I 183
 GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGGCTCCAAT 661

TAGCACCTATAGGAGTATTGCATGGGCTTCAAGGAAACTTCTACATTATTATTATGA 721

TACTGTTCTGTACTGTTATTCCCTTTTATGGTCTTCTTGAGACTTAAGTTGTAGAATTA 781

AATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG 820

FIG. 15D

GAGCTCCGAGCCCTCtCTGGCGCgCgAGGTATTTCTGTCTGTnCCCCGGGGTGCACAGTGA 60
 GCCCCAGCGGATCCGGAGGGTAAGCTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC 120
 AAGCTTCGCCCTCTGCGTCCCCCGGCCCTTCGCGGTCTCCCGCCAGTGCAGGTCCGGGGCC 180
 CCCAGGCGAGCGGACAAAGTTGGCCCTAATCTGCCAAACTTCTGGGGCATTTACCGTGCTC 240
 TGGCCGCCCTCCCGATTCTTCCCTCCCGGCCCTTGCCCTGCTTCTCGCCFACCCCGGGCTC 300
 CGGAAGGGAAGGAGGCGTGTCCGGAGCAGGGCGGGGAACTGTATAAAAGCGCCGGCGG 360
 CTCAGCAGCCGGCTTCGCTCGCCGCCCTCGCGCCGAGACTAGAAGCGCTGCGGGGAAGCAGG 420
 GACAGTGGAGAGGGCGCTGCGCTCGGGCTACCCAAATGCCGTGGACTATCTGCCCGCGCTGT 480
 TCGTGCAATCTTGGAGCTCCAGAACACAGCTAAACGGAGTCGCCACACCACTGTTTGTGC 540

-25 -21
 MetLysLysThrGln

TGGATCGCCTTCCCTTATGAAGAAGACACAAAGTGAGTAGGGCGGCCCGGGA 600
 GCTCCCAGGCTCTCCAGGAAAAATCGCGCCCGGTGCCCGGGGAAGCCGGCTCCCTGG 660
 GACTTGCAGCTGGGGGTGCAGGGCTGTGCCTGCCGGGTGAGACAAGAGGATGCGGGGGA 720
 GGCCGGCGTGTGTGATCCCCGAGCCGAGCCGnnTGAGCCAGGGAGAAAAGGAGTGGGA 780
 GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCCTCAGCAGTTAAGTTTGTAGCTGTGAG 840
 TCGGAAACCGTAAATTCCTGCTGTTGGAAAGATTGGCTTTnGCCACGGAATGTAAGTT 900
 ATCAC 905

FIG. 15D CONT.

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTACAGTGTAATAAGGAA	60
AAATAAGTCATGCATAAAAGCAACTATAATAFACATAAGAAAATGTTATTTCAAAGCCGA	120
TGTGTAGGTTATGTGTGTTTCGAGAGAGAGAGAGAGACAGATTACTTTCTGCTAGGGT	180
TCAAGAATGCCCTTCCFTGTTGGCTAAGGAAATATTTCTTAAGTGGCTAAAAAGCTGTGT	240
TTCAAAAATATTTCTTTTGATGTCCTCACAAATTCAGTGGAAATCTCTTAGGCTAAAAAATAT	300
ACATCTCTCTCACCTTTAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA	360
GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAAAATAAGATGTTTCTTT	420
TGGTGCCATAAGGTATACATTTTATGCATTCTCTAGTTTGTAGAAGATACCCCTAAGGGCT	480
AAGTCTTTAACAATGCTGTACAAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA	540
AAGTTTTTAACAAGTTAACAATATTGTTCATTGAGAGAAATAATTCAAAATGGATTTTAA	600
CTAAAAGCTTTTAAAAAACTTTGGTGAGCATAGCTTGAATGCGTAATATTAAATTGCATTT	660
AAGCCAATAACATATATTAGACTGGTCTTTTGTGTCATCAAGGCATTAGATGTTAAAGT	720
-20	
TTGAATGATTACAGATCTTAACTGATGATCACCACCAAGCAATTTTCTGTGTTTTCATTTAGAC	780
Th	
rTrpIleLeuThrCysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG1	
TTGGATTCTCACTTGCAATTTATCTTCAGCTGCTCCTATTAAATCCTCTCGTCAAAACTGA	840

FIG. 15D cont.

1 uGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeu 18
 AGGGATCTGCAGGAATCGTGTGACTAATAATGTAAGACGCTCACTAAATTGGTAAGTAA 900
 GGAATGCTTTACCGTGCTGTGTAAAAAGAGAGCTGTGGCTCTTTTTCCTGTGCTTGTGAT 960
 AAAAGATTTAGATTTTCTTGCCCCAAAGTAATGTTTTCCTAAAGTGGGAAAGTAATCA 1020
 CTGGGTTTACAATAAAGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA 1080
 TTTGTTGGTAAAACTGGCTAGTTGCACACCAGTCTGTGACTGCTTCTTTGCTGGTCTTC 1140
 TCCCCATCCTTCATAGGCAGTGAAGGACCTTGGAGAGTTCGCTGTGTGCTGATGGGCTTG 1200
 CCCCAGCTTGTTCCCCATAATCTCTCCAGTGGGTTTCCCAGCATGTCTATTTCCCTTCA 1260
 CATGTCTTCC'FACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCTGAAATGGCTATTCTC 1320
 CCAATTCAATCAGCAGGAAGACCCCTGTACATGTGAGTGGGTGTTTGTCTCCTTCAGGGAA 1380
 CATAGAGAGGCTGATTTCATTGCCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTACAT 1440
 TGAAC'TCTTCCCTCAGCGAAAGCATTTGTCATTGCTTCCC 1479

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGGTGAAATTCAGATCATGTTTCCAAAACCTCAGTAGGT 60
 TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAAGATCTGTATTATCACTTTTITA 120
 TTTTGAAGGATGCCCTTTTGATTACAGAGGGGAAATCAAGGATTAAAAATCAATATACATGT 180

FIG. 15D CONT.

AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAAACAGTTTGTGTGCTTTTCTCTCAA 240
 AGCACTACAAATATGATTAAATTGATGTATAAGAAATTTCTTATGGAAATTTTCTTTTGTGT 300
 19
 ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM 30
 CTCTGTAGGTGGCAAACTCTCCAAAAGACTACATGATAACCCCTCAAAATATGTCCCCGGGA 360
 39
 etAspValLeu
 TGGATGTTTGGTATGTAAACTACATTTCTGAGTTTTCATTTTAGTAGCTCATAGAAGAAA 420
 TGGGATCATTCATATGAGATAGTACACTAGCTGCTATTTAGGAGCTTGCTTATTGTCAG 480
 GATTGAAGAATTTATCTTTGGAAATTGACTTGCAGGCTTTTTTCCCCCTCTT 535

Intervening sequence of unknown length

CCTGTTACAAATCTCCCTCCTCTATTACAAATAGTCCCTCCTCCTGTCACTAGTC 60
 CCTTCTCTCTCTGTTACAAATAACCCCTGTCTCCTCTATTACAAACATTTTAAAGTAATGTAAT 120
 ATTAATTTTAAAAATCTGGCCAGGCACGGTGTCTCATGTCTTGTAAATCCCAGCACATTGGG 180
 AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCTGGCCAAACATGGT 240
 GAAACTTCCTCTCTACTAAAAATAAAAAAGTAGCCAGGCATGGTGGCAGGCACCTTGTAAT 300
 CTGAGCTACTCGAGAGGCTGAGGCAGGAGAAATCACTTGAGTAACATAAACGATAGCTTTG 360
 AAGAGTACTCCGAGTTTATATGGCACTTACTTATTAATAATAGCTGTTTGTCTCTTTTTC 420

Intervening sequence of unknown length

euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
TGACTGATCTTCTGGACAAGTTTTCAAATATTCTGAAGGCTTGAGTAATTATCCATCA

leAspLysLeuValAsnIleValAspLeuValGluCysValLysGluAsnSerL
TAGACAAACTTGTAATATAGTGGATGACCTTGTGGAGTGCGTGAAAGAAACTCATCTA

ys
AGGTAACTTGTGTTCA**TTGGG**ATTATTTTCA**TTACG**CTCTCTAA**AAACCC**ATGCTTC
660

TTGGTGCTGTTGGGAAAATGAGGCACCTTTATTTATGATATTTGATTGTATAAAGCTTC 720

AAATTTAAAAATCTTGTTCAGATGAGCAAGAAAACAAGTATTGCAGTTATCTGCAAT 780

ACTGAAGTGCACATTC

Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCACTACCCCTGCATTACC 60

AAATCTGAATTACATACGTTAAACAGCCATCTAAAAGTGCTAGTTGTAAGAGTCTAAATA 120

CTTGAATCTTTGAGAGACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA 180

97
AspLeuLysLysSerPheLysSerP
CTATTGAAAAATGTAACTCCTATTTTCTCTAGGATCTAAAAAATCATTCAGAGCC 240

110 roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspa
 120 CAGAACCAGGCTCTTTACTCCTGAAGAATTCTTTAGAAATTTTAAATAGATCCATTGATG 300
 130 laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS
 140 CCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTTGTGGTTTCTTCAACATTAA 360
 148 erProGluLysA
 GTCCGTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTAAACAACAACTTAAA 420
 TCTTCCCCTATGTAGTAAGAATCTACCTCTGTGTAAAGCTGTAGCAAGATACATGCATGTA 480
 CGTCTAATAAAAAAGCAGATATCAATAGCACAGAAAGAACTAATGATTGTAGATTGTGGG 541

Intervening sequence of unknown length

CTCTATAACTCATACAAATCACCATATATAACACTGACACATTATTGCTTTCTATTAGATT 60
 150 spS
 erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA
 160 CCAGAGTCAGTGTACAAAACCATTTATGTTACCCCTGTTGCAGCCAGCTCCCTTAGGA 120
 170 snAspSerSerSerSerAsna
 ATGACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTAAATGCATGGCTCCA 180
 ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTATTATTATT 240
 GATACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAAGTTTGTAGAAT 300

FIG. 15D CONT.

TAAATTCCCTAGAGCTGGAGATAATGTTTAGAGAAATTAGGCCAATAAATTTCTGCTGA 360
GGTTATTTTAAATAAGACATAAAATAATTTTAGAAATATGATTATGCCTTTTGTGAA 420
TCATTAACATATAT 434

Intervening sequence of unknown length

ACAGAAACAGTTAAACAACCCACAGCATAAGAGAAAACTTCTAGAATGGATATGCTGTA 60

178

TTCATCAGTGTGTTCTTTAAATTATAGGGAAGGCCAAAAATCCCCCTGGAGACTCCAGCC 120
rgLysAlaLysAsnProProGlyAspSerSerL

190

200

euHisTrpAlaAlaMetAlaLeuProAlaLeuPheSerLeuIleIleGlyPheAlaPheG 180
TACACTGGGCAGCCCATGGCATTGCCAGCATTTGTTTCTCTTATAAATTGGCTTTGCTTTTG

213

lyAlaLeuPhePhePheLys 240
GAGCCTTATAC'TGGAAGGTAAGTGGTACCATTCCCTTTTAAAAAATATGCTATGTCTAC

ATAAAATTATCATCTTTTTTTCCTCAAGAAATGATCCTTAAAGAAAACAGTGAATCTACCT 300

TAGCTTATACTAAACAAAATTTAAATTTTATAAAGTTTCCTGTTTCTCATTTATGTCTGGA 360

GACAATCCCCTCTAGCTGATAATTCACGCTTAAGAATTAGGAACT 404

Intervening sequence of unknown length

FIG. 15D CONT.

AAAACTGTTATTGGAGTTATTGCCATAAAAGATAAAAGTGGAGTCCACTTACCTCTTAAA 60
 214
 TATTAGACCATTTCATTGATTATTTTACAGTATATGTCTTTCTTCTTTTCCAGAAAGAGAC 120
 LysArgG
 220
 InProSerLeuThrArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIleS 235
 AGCCAAGTCTTACAAGGGCAGTTGAAAATATACAAATTAATGAAGAGGATAATGAGATAA 180
 e
 GGTATTTTGTTTTGCTAAATGTGTgCCCAATCAAGCATGACATTGCCATTTCACACACTG 240
 TGTACCTGCCCATAAATGTCTTTAAAGAAGTCCTTCACTCATGACAGTAGCTCCTAACCAGT 300
 GAGTCCCAACTCTATCCATGTTTCTGTGATGTCTCACTCTCTCTTC 344
 Intervening sequence of unknown length
 GTATGTGTATATGCATATACAGAGAAAGAAATGTTTAACTACTTGGAAGACTACCTTA 60
 AGACAAATGAAGTCTTCCCTCTTCCCTATAGTAATAAGAGGTAGGCTCCCCCATTCAT 120
 TTTGCAATCTTCTGCTACTATATTTACAGAAAAGCTGCCTTTTACAATGCCGAGATCATG 180
 GTGTACCTCAGAATCTCTGACCAAGAGCAAAATAAGCATTTTCTTATTGTTTTTCAGTA 240
 237
 etLeuGlnGluLysGluArgGluPheGlnGluVal 248
 TGTGCAAGAGAAAGAGAGAGAGTTTCAAGAAAGTGTAATTGTGGCTTGATCAACACTGT 300
 TACTTTCGTACATTGGTAAAGTTTTTTTCTCTTCTTCTTTTCTTTTCTTTTATTATA 360

FIG. 15D CONT.

CTTTAAGTTCTAGGGTACATGTGCACAATGTGCAGGTTTGTACGTA TGTTTACATGTGC 420
CATGTT 426

FIG.16A

-25
 Human MKKTQTWILT CIYLQLLFN PLVKTEGICR NRVTNVVKDV TKLVANLPKD 25
 Monkey MKKTQTWILT CIYLQLLFN PLVKTEGICR NRVTNVVKDV TKLVANLPKD
 Dog MKKTQTWIIIT CIYLQLLFN PLVKTKGICG KRVTDVVKDV TKLVANLPKD
 Cat MKXTQTWIVT CIYLQXLLFN PLVKTKGLCR NRVTDVVKDV TKLVANLPKD
 Cow MKKTQTWIIIT CIYLQLLFN PLVHTQGICS NRVTDVVKDV TKLVANLPKD
 Rat MKKTQTWIIIT CIYLQLLFN PLVKTQEICR NPVTDNVKDI TKLVANLPKD
 Mouse MKKTQTWIIIT CIYLQLLFN PLVKTKEICG NPVTDNVKDI TKLVANLPND
 Chicken TWIIIT CFCLOQLLLN PLVKAQSSCG NPVTDDVNDI AKLVGNLPND
 Scfpep MKktQTWIIIT CIYLQLLFN PLVkt.gicr nrVtd.VkDv tKLVANLPkD

26
 Human YMITLKYVPG MDVLP SHCWI SEMVQLSDS LTDL LDKFSN ISEG...LSN 72
 Monkey YMITLKYVPG MDVLP SHCWI SEMVQLSDS LTDL LDKFSN ISEG...LSN
 Dog YKIALKYVPG MDVLP SHCWI SVMVEQLSVS LTDL LDKFSN ISEG...LSN
 Cat YKIALKYVPG MDVLP SHCWI SVMVEQLSVS LTDL LDKFSN ISEG...LSN
 Cow YMITLKYVPG MDVLP SHCWI SEMVEQLSVS LTDL LDKFSN ISEG...LSN
 Rat YMITLNYVAG MDVLP SHCWL RDMVTHLSVS LTLL LDKFSN ISEG...LSN
 Mouse YMITLNYVAG MDVLP SHCWL RDMVIQLSL S LTLL LDKFSN ISEG...LSN
 Chicken YLITLKYVPK MDSLPNHCWL HLMVPEFSRS LHNLLQKFSN ISEG...LSN
 Scfpep YmitLkYVpg MDvLPsHCwi semveqlsvs LtdLldKFSn Iseg...LSN

73
 Human YSIIIDKL VNI VDDLVECVKE NSSKD.LKKS FKSP EPRLFT PEEFFRIFNR 121
 Monkey YSIIIDKL VNI VDDLVECVKE -NSSKD.LKKS FKSP EPRLFT PEEFFRIFNR
 Dog YSIIIDKL VNI VDDLVECTEG YSFEN.VKKA PKSP EPRLFT PEEFFRIFNR
 Cat YSIIIDKL VNI VDDLVECVEG HSSEN.VKKS SKSP EPRLFT PEEFFRIFNR
 Cow YCIIDKL VNI VDDLVECMEX HSSEN.VKKS SKSP EPRQFT PEKFFGIFNK
 Rat YSIIIDKL GKI VDDL VACMEE NAPKN.VKES LKKP ETRNFT PEEFFSIFNR
 Mouse YSIIIDKL GKI VDDLVL CMEE NAPKN.IKES PKRP ETRSF T PEEFFSIFNR
 Chicken YSIINNLTRI INDLMACLAF DKNKDFIKEN GHLYEEDRFI PENFFRLFNS
 Scfpep YsiIdkLvkI vddlveC.ee nsskn.vKks .kspeprlft PEEFFRIFNR

FIG.16B

122 Human SIDAfKDF.V VASeTSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR 169
 Monkey SIDAfKDF.A VASeTSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
 Dog SIDAfKDLET VASKSSECvV SSTL.SPDKD SRVSVTKPFM LPPVAASSLR
 Cat SIDAfKDLEM VASKTSECvV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
 Cow SIDAfKDLEI VASKMSECvI SSTs.SPEKD SRVSVTKPFM LPPVAASSLR
 Rat SIDAfKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
 Mouse SIDAfKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
 Chicken TIEVYKEFAD SLDK.NDCIM PSTVETPEND SRVAVTKTIS FPPVAASSLR
 Scfpep sIdafKdf.m vaektSDCvV sStl.sPeKD SRVSVTKPfm LPPVAASSLR

170 Human NDSSSSNRKA KNPPGD.... ..SSLHWAAM ALPAFFSLII GFAFGALYWK 213
 Monkey NDSSSSNRKA KNPTGD.... ..SSLHWAAM ALPAFFSLII GFAFGALYWK
 Dog NDSSSSNRKA SNSIGD.... ..SNLQWAAM ALPAFFSLVI GFAFGALYWK
 Cat NDSSSSNRKX TNPIED.... ..SSIQWAVM ALPAFFSLVI GFAFGALYWK
 Cow NDSSSSNRKA SNSIED.... ..SSLQWAAV ALPAFFSLVI GFAFGALYWK
 Rat NDSSSSNRKA AKSPED.... ..PGLQWTAM ALPALISLVI GFAFGALYWK
 Mouse NDSSSSNRKA AKAPED.... ..SGLQWTAM ALPALISLVI GFAFGALYWK
 Chicken NDSIGSNTSS NSNKEALGFI SSSSLQGISI ALTSLLSLLI GFILGAIYWK
 Scfpep NDSSssNRka .n..ed.... ..sslqwaam ALpalfSLVI GFafGALYWK

214 Human KRQPSLTRAV ENIQIN...E EDNEISMLQE KEREfQeV 248
 Monkey KRQPSLTRAV ENIQIN...E DDNEISMLQE KEREfQeV
 Dog KKQPNLTRTV ENIQIN...E EDNEISMLQE KEREfQeV
 Cat KKQPNLTRTV ENIQIN...E EDNEISMLQE KEREfQeV
 Cow KKQPNLTRTV ENRQIN...E EDNEISMLQE KEREfQeV
 Rat KKQSSLTRAV ENIQIN...E EDNEISMLQQ KEREfQeV
 Mouse KKQSSLTRAV ENIQIN...E EDNEISMLQQ KEREfQeV
 Chicken KTHPKSRPES NETIQCHGCQ EENEISMLQQ KEKEHLQV
 Scfpep KkqpSltrav eniqin...e edNEISMLQe KEREfQeV

FIG. 16C

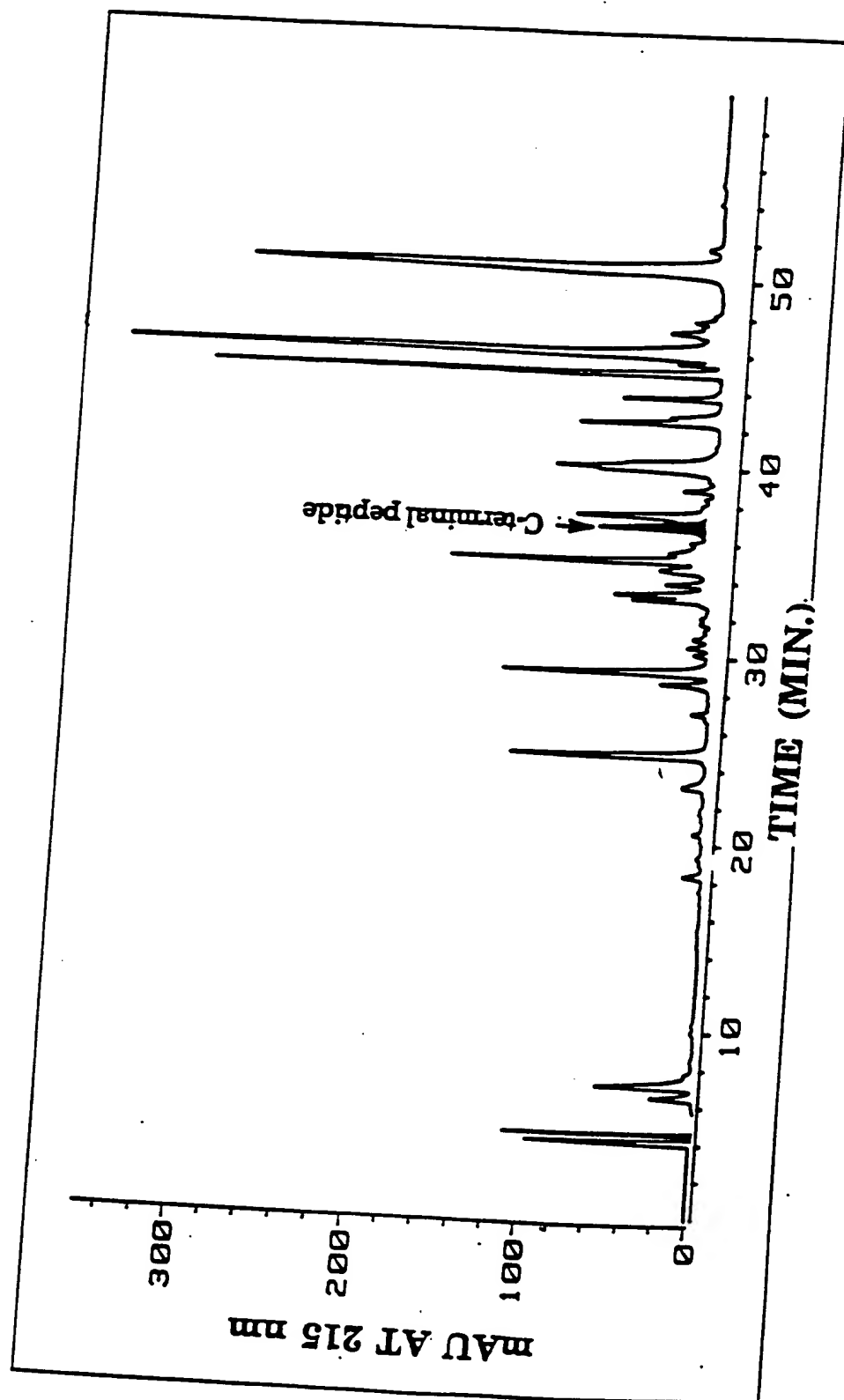


FIG. 16D

EcoRI

ta a t t t a a t t c g t a
GAATTCTTCCGTATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT
 E F F R I F N R S I D A F K D F V

g a t tagt t t g t a at a ag t g
 GTTGCTTCCGAAACCTCCGACTGCGTTGTTTCCTCCACCCTGTCTCCGGAA
 V A S E T S D C V V S S T L S P E

BstEII

t a a cagt c a a t t a c t . a
 AAAGACTCCCGTGTTTCGGTTACCAAACCGTTTCATGCTGCCGCCGGTTGCT
 K D S R V S V T K P F M L P P V A

cag tag t ag agtag agt tagt g a t
 GCTTCCTCCCTGCGTAACGACTCCTCCTCCTCCAACCTCCAAATACATCTAC
 A S S L R N D S S S S N S K Y I Y

BamHI

t
CTGATCTAATAGGATCC
 L I . .

FIG 16E

BstEII
GGTTACCAAACCGTTCATGCTGCCGCCGGTTGCTGCTTAATAGGATCC BamHI
V T K P F M L P P V A A . .

FIG.17

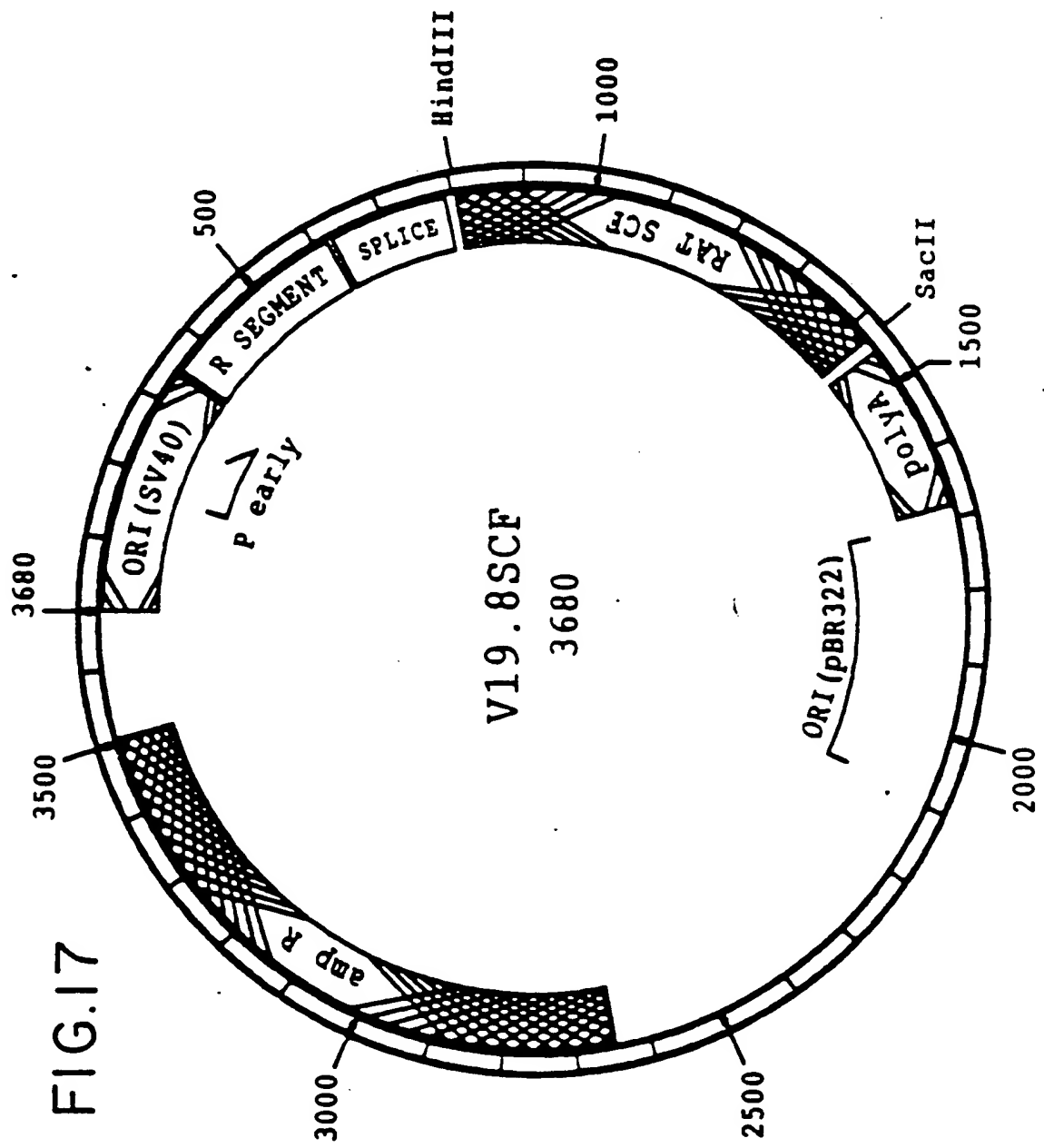
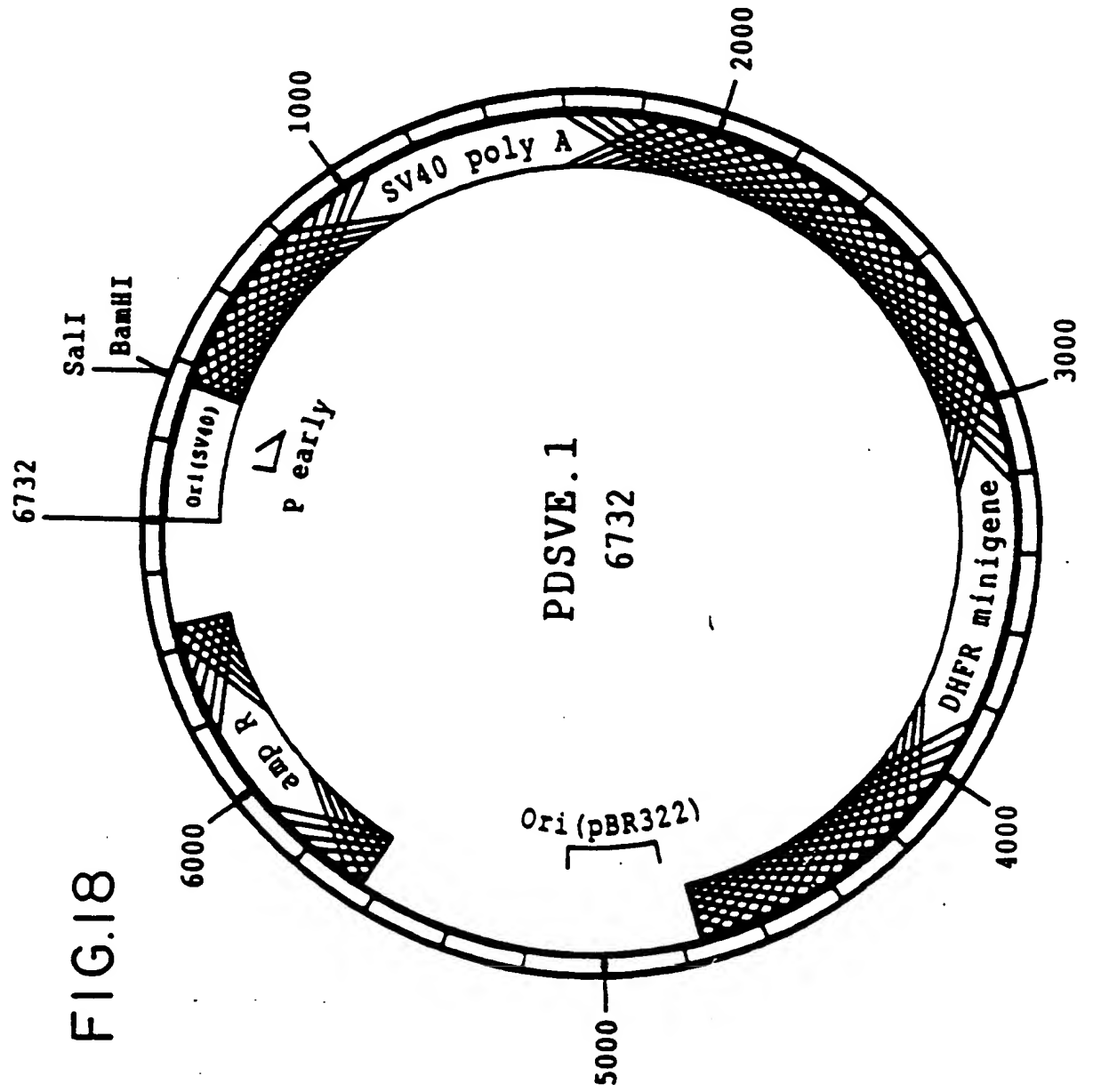


FIG.18



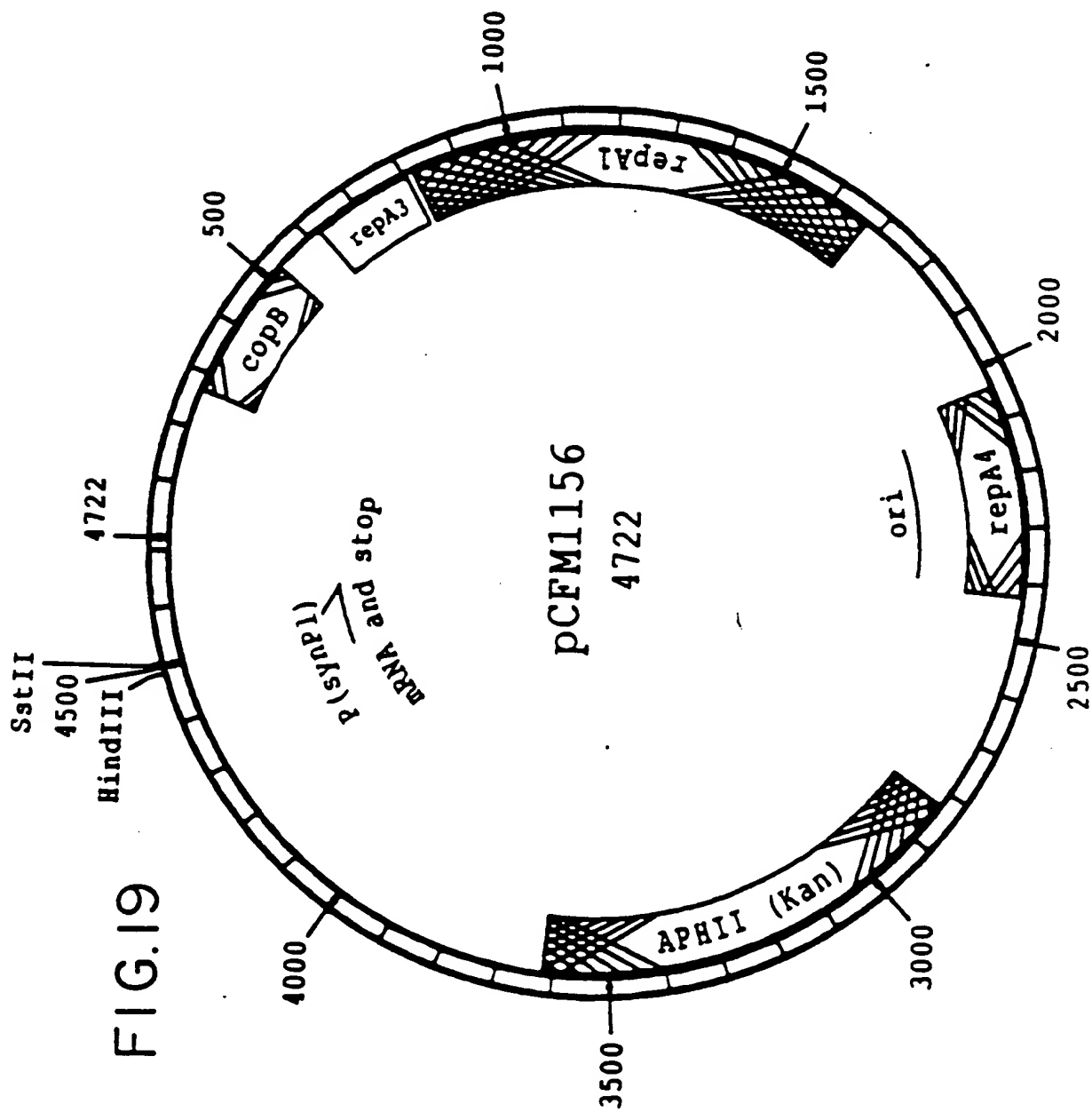


FIG.19

FIG.20A

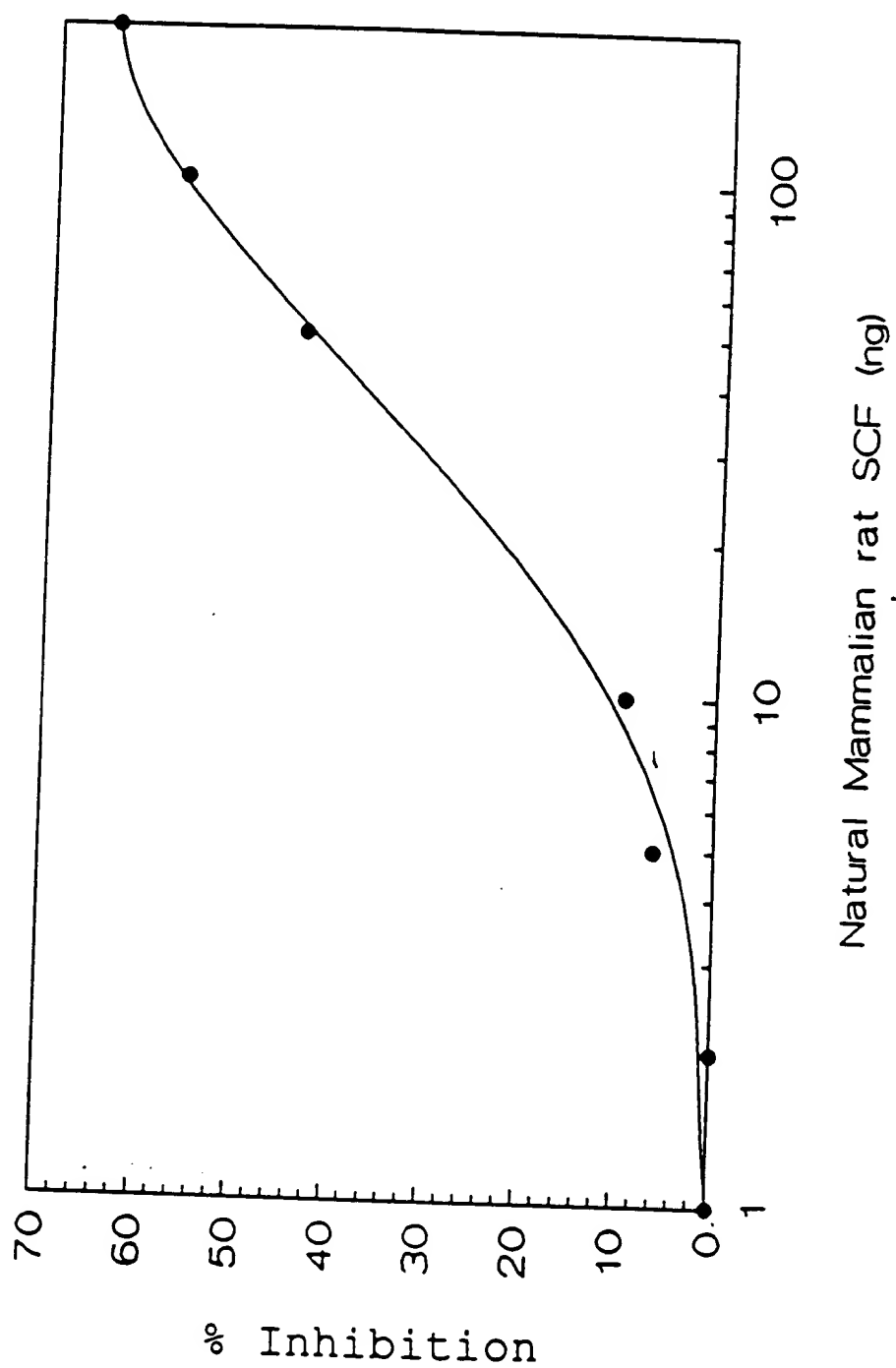


FIG.20B

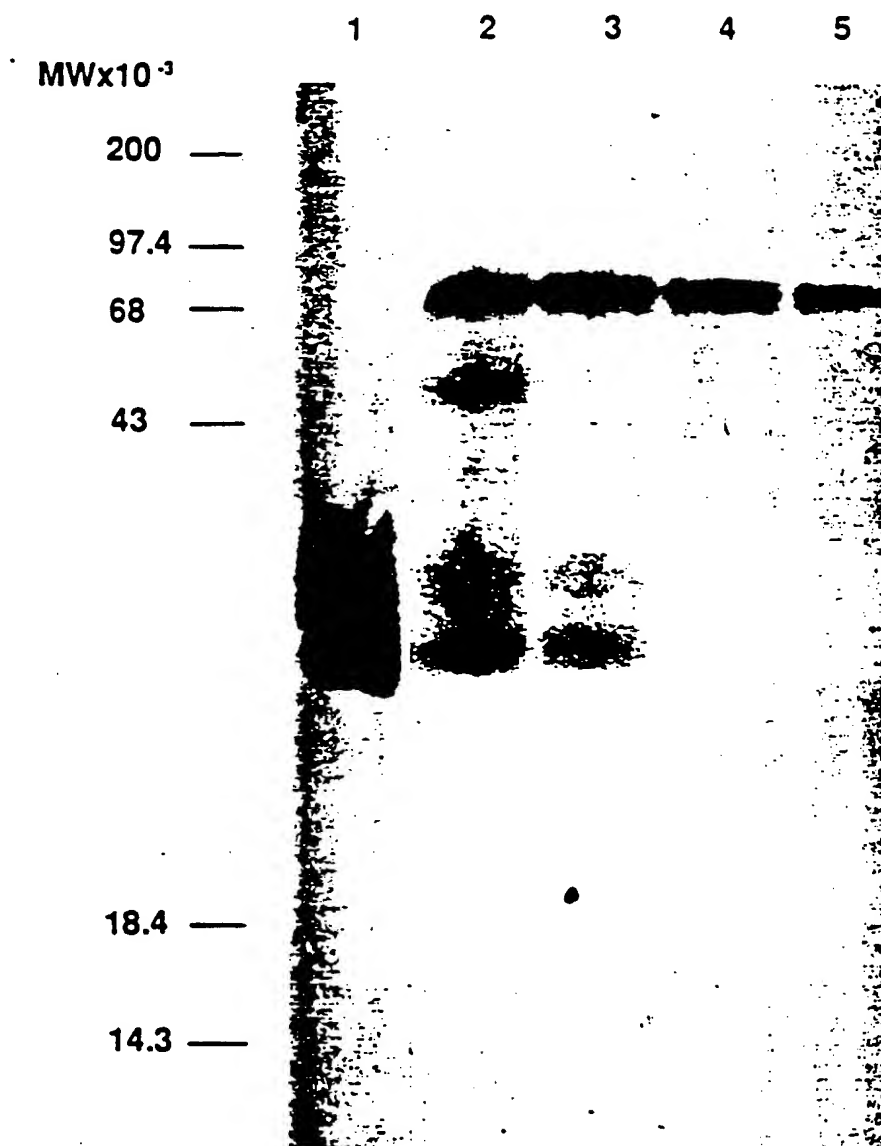


FIG. 21

1 2 3 4 5 6 7 8 MWx10⁻³



— 43

— 29

— 18.4

— 14.3

— 6.2

FIG.22

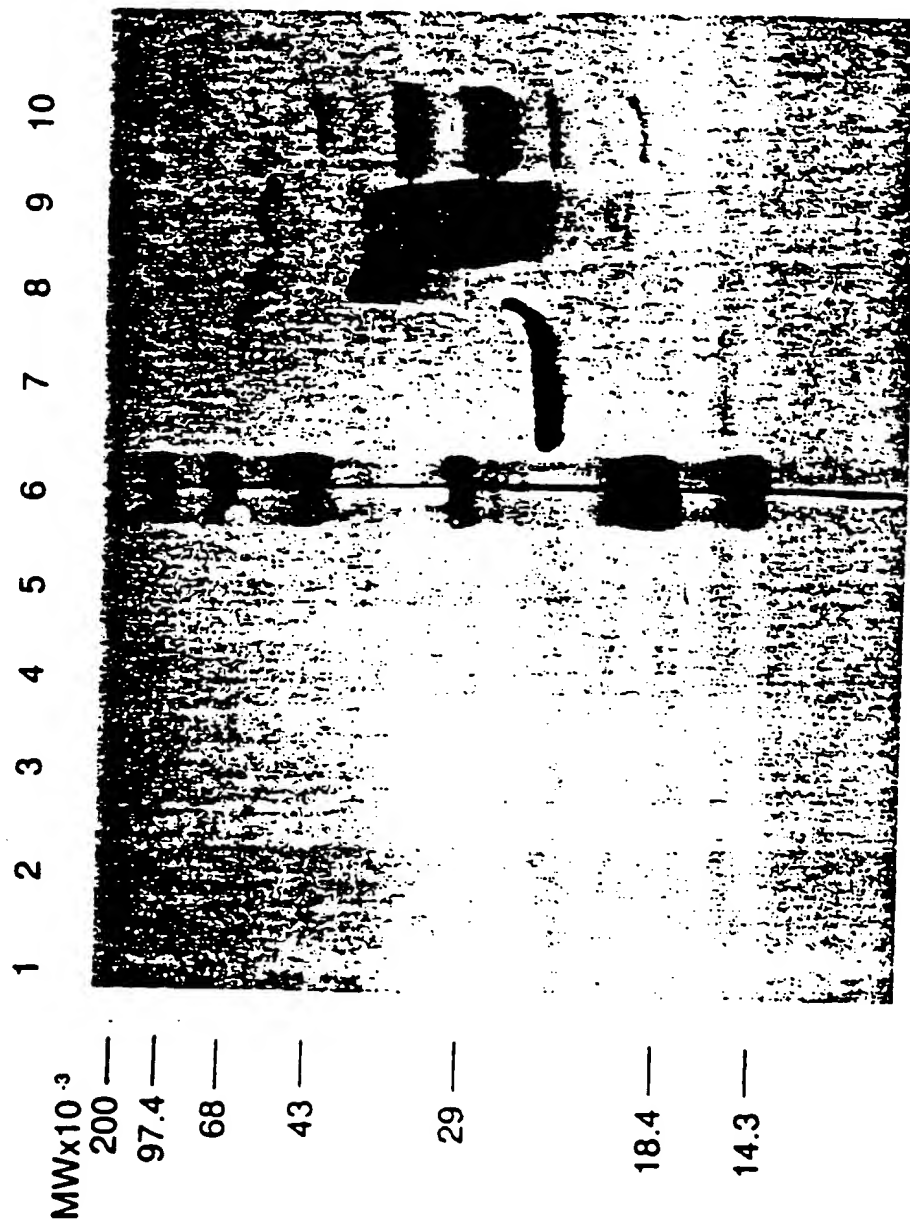


FIG. 22A

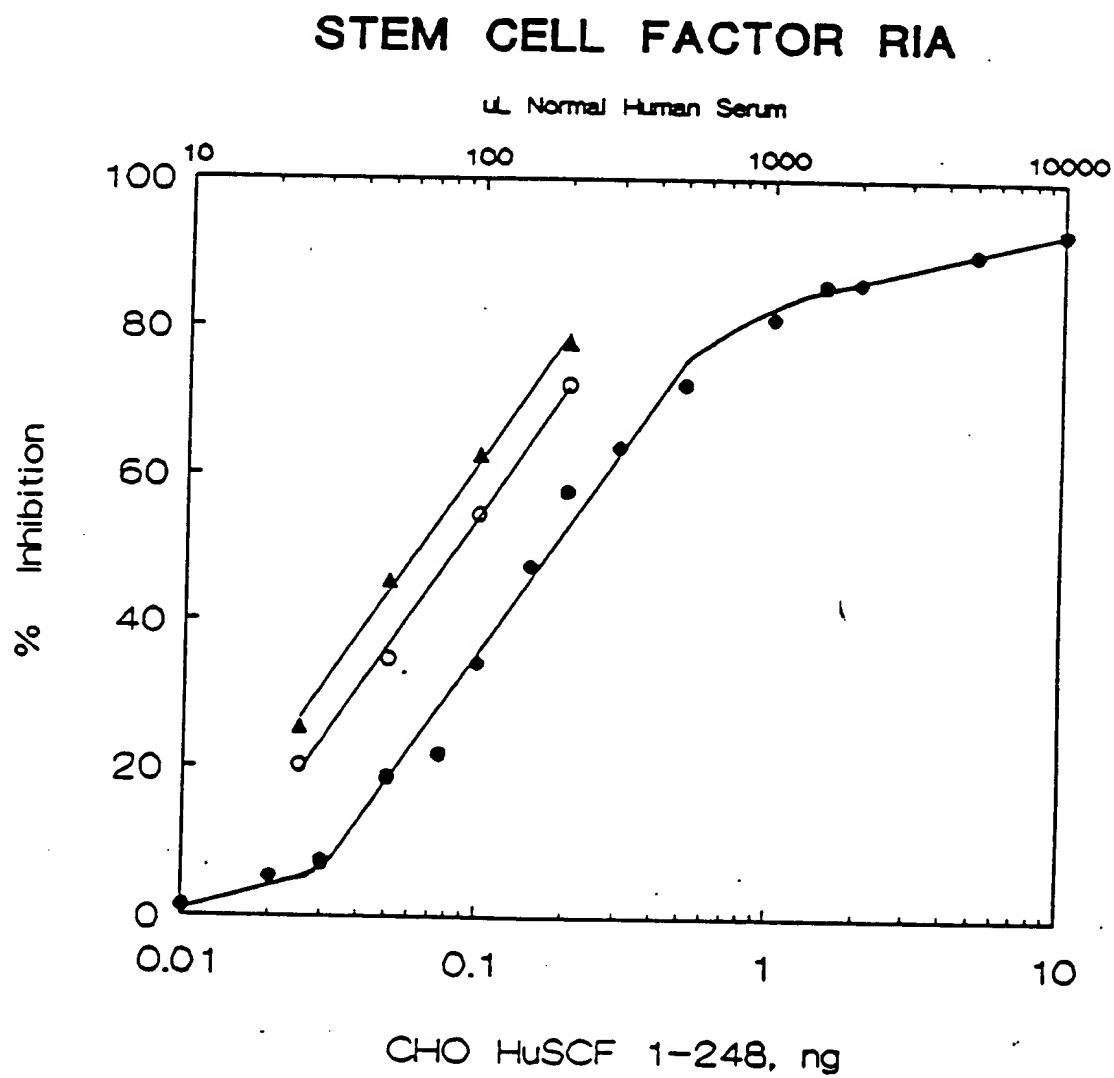
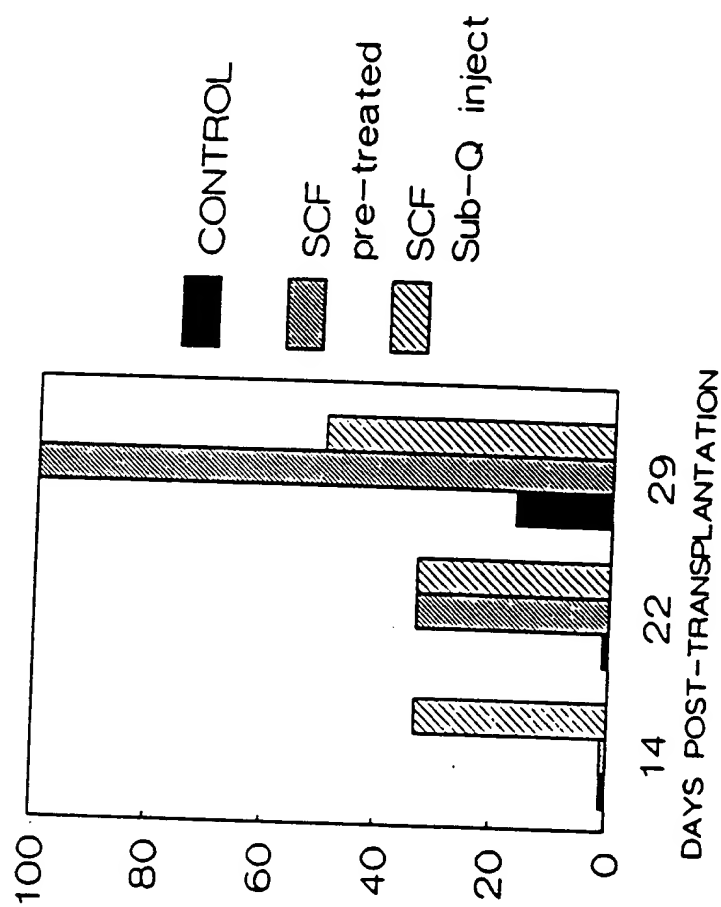


FIG. 23



% MICE CONVERTED TO DONOR PHENOTYPE

FIG. 24A

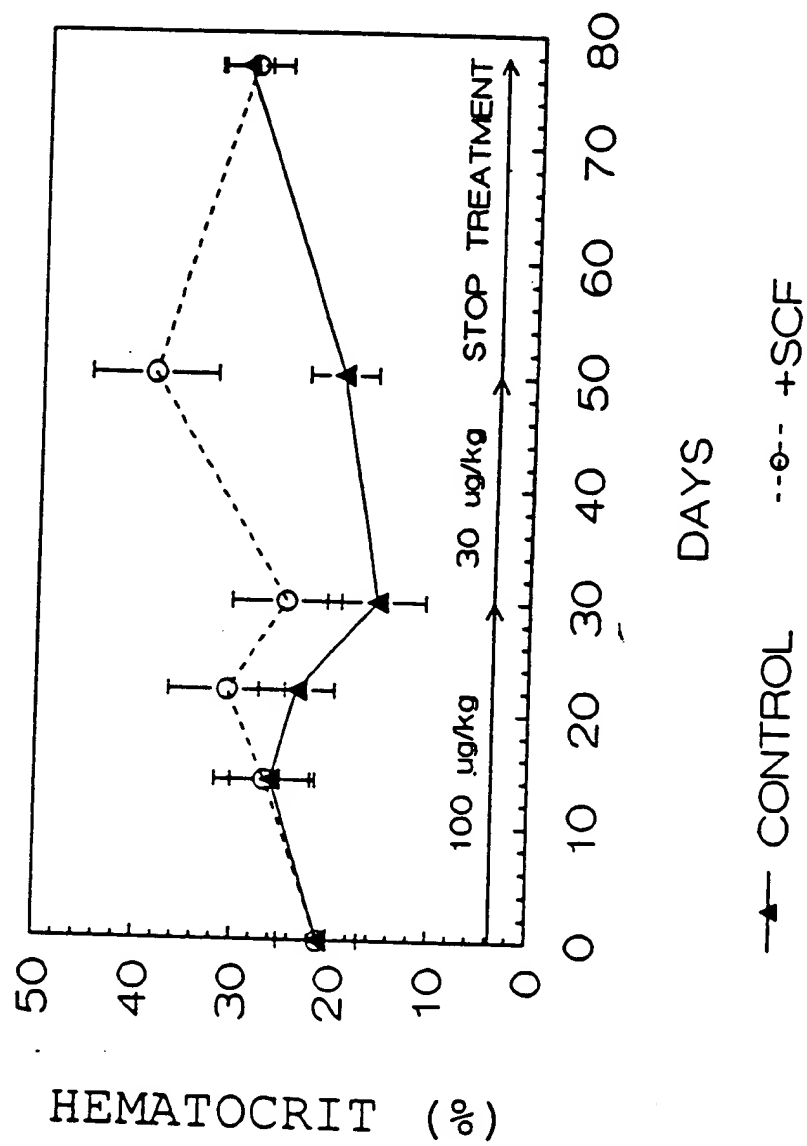


FIG. 24B

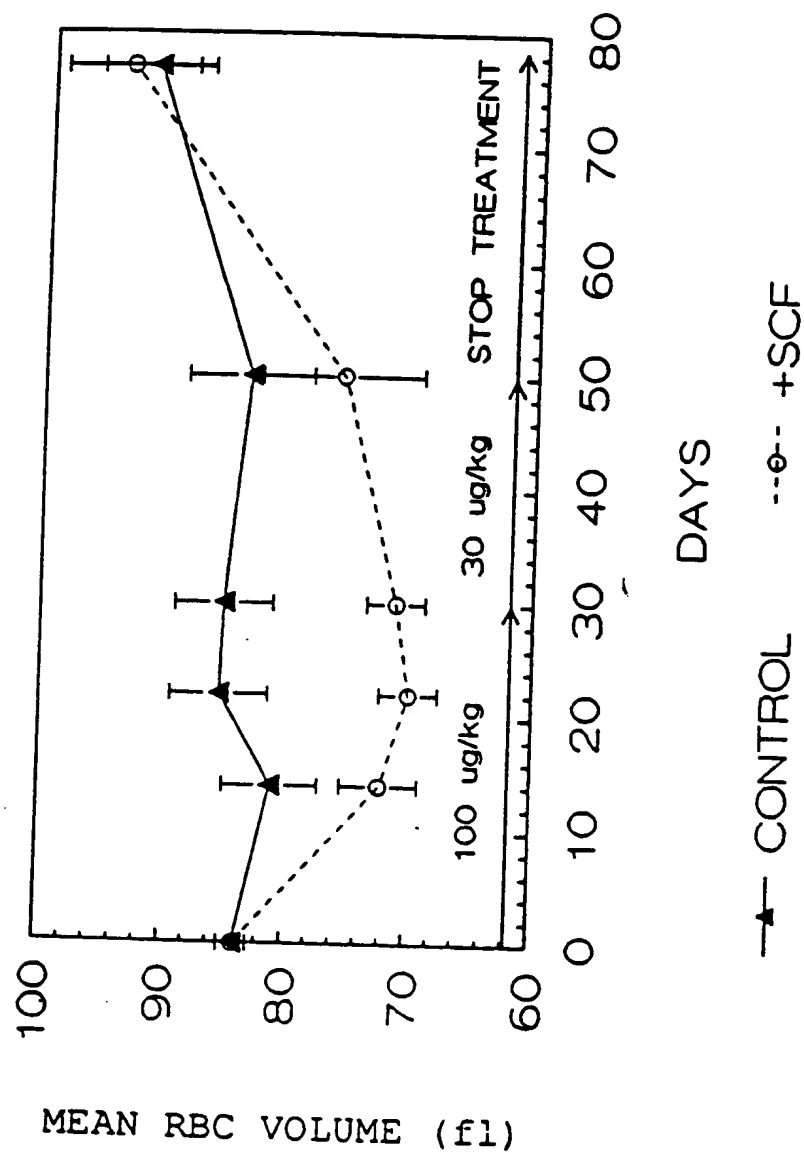


FIG. 25

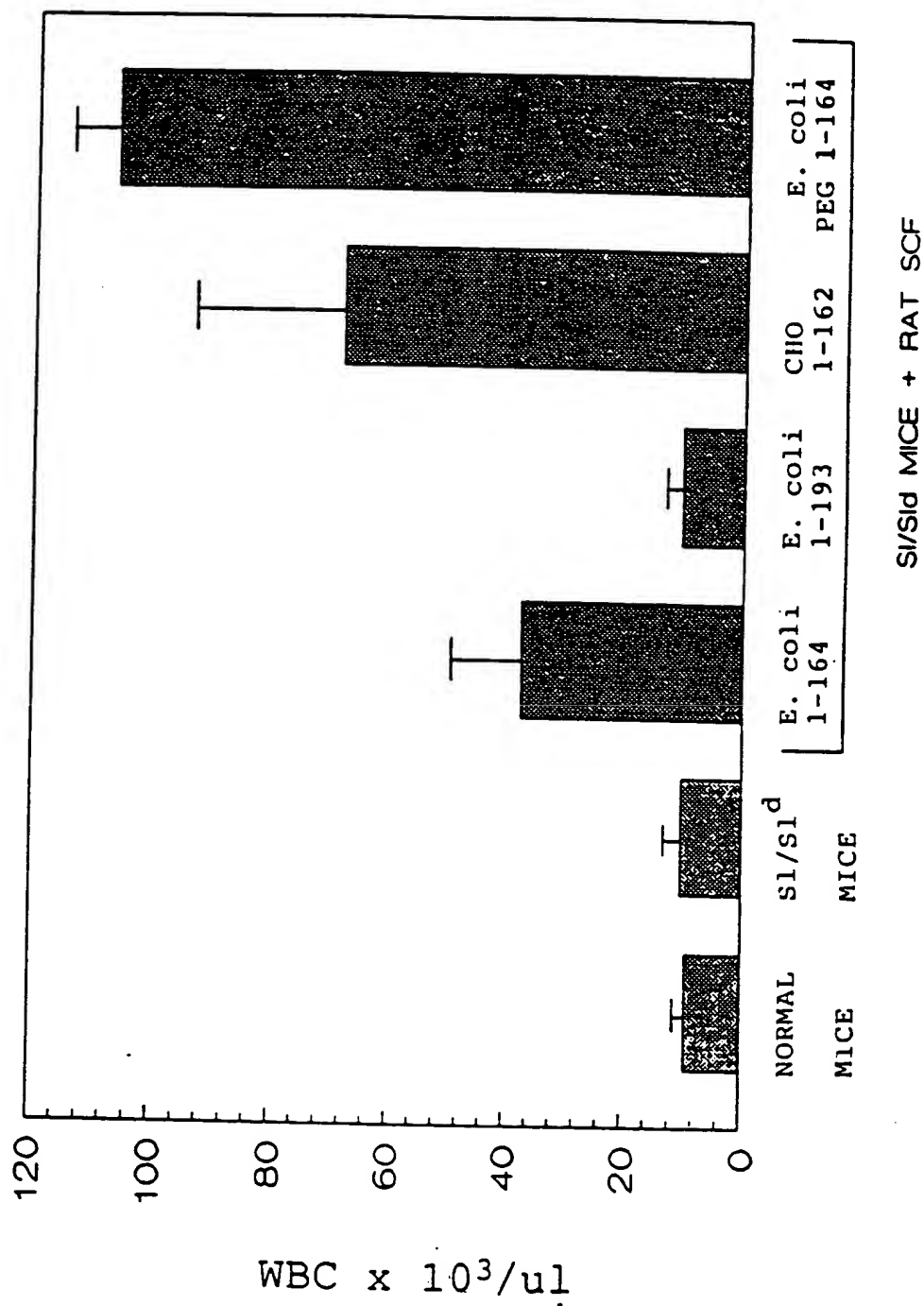


FIG.26

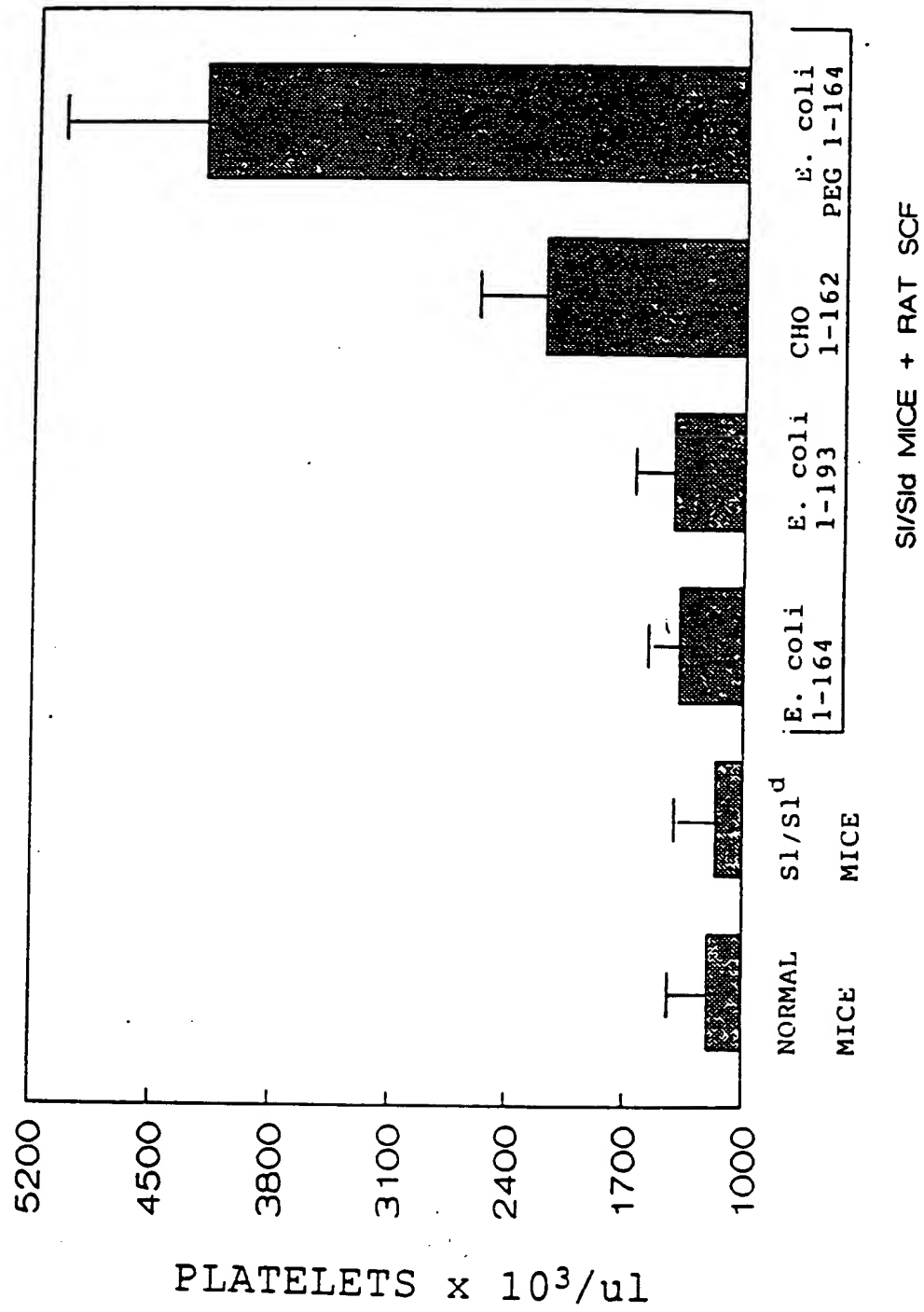


FIG. 27

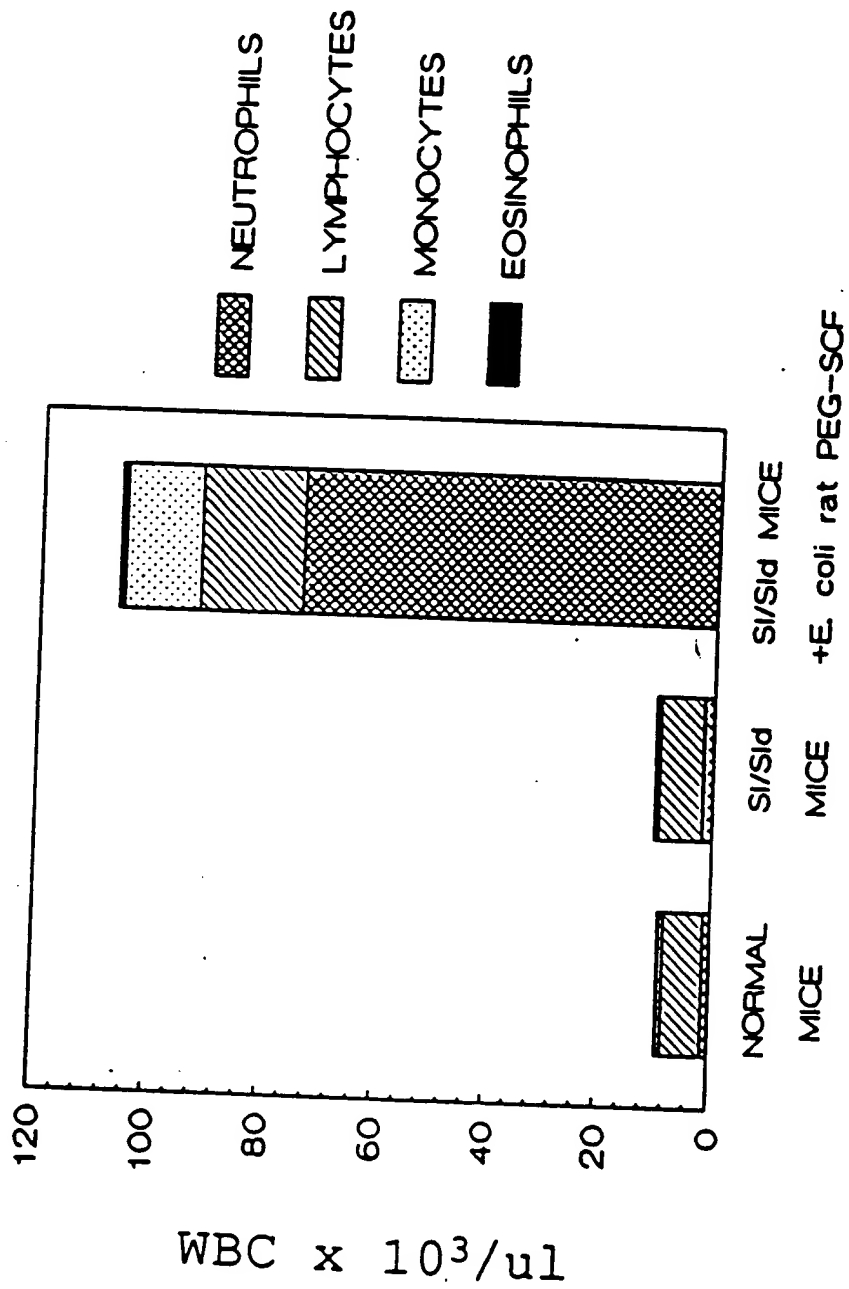


FIG. 28

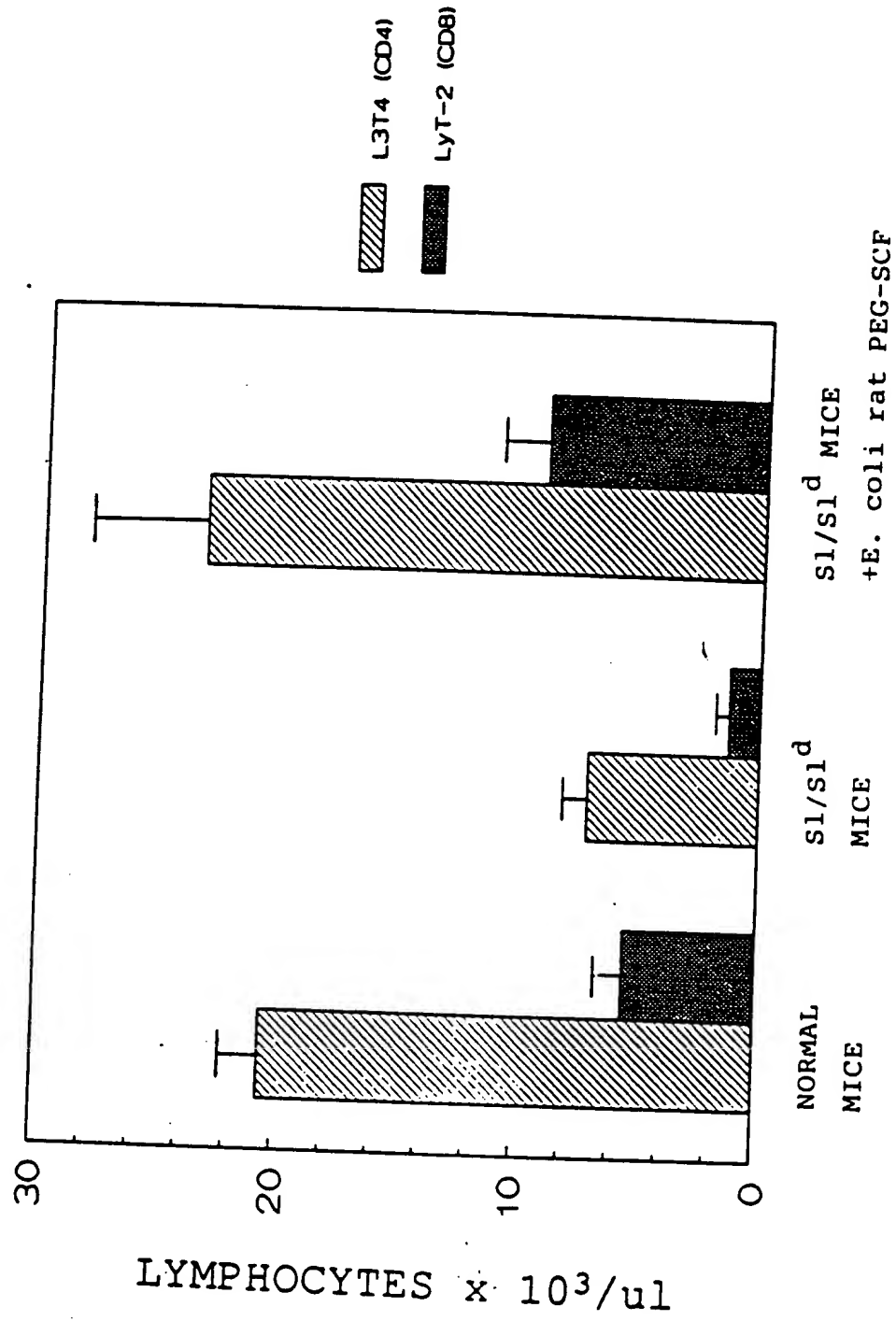


FIG.29A

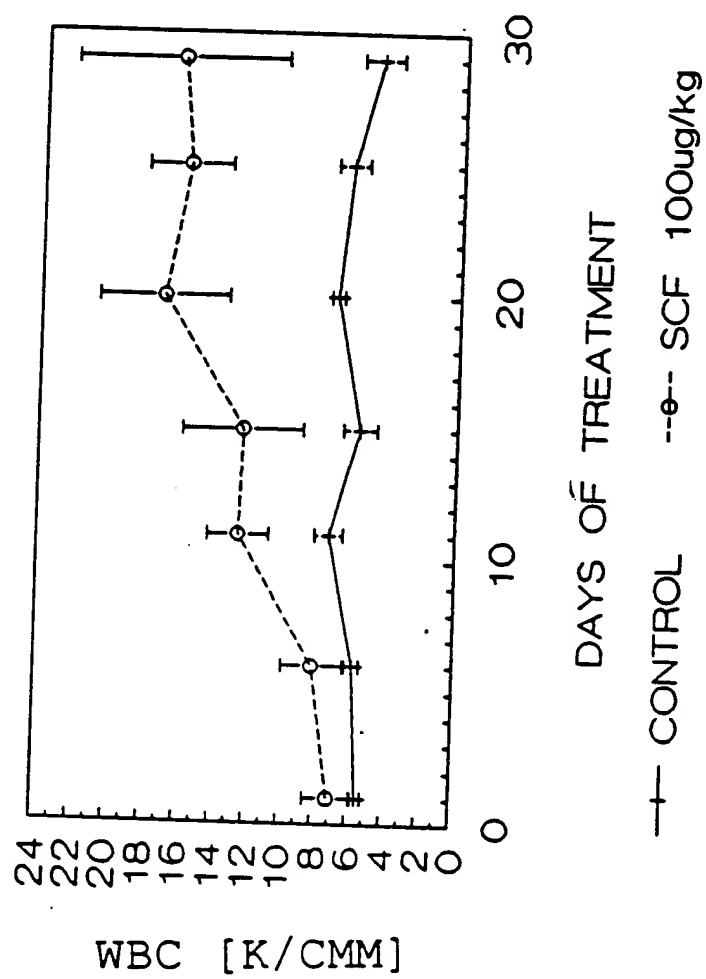


FIG. 29B

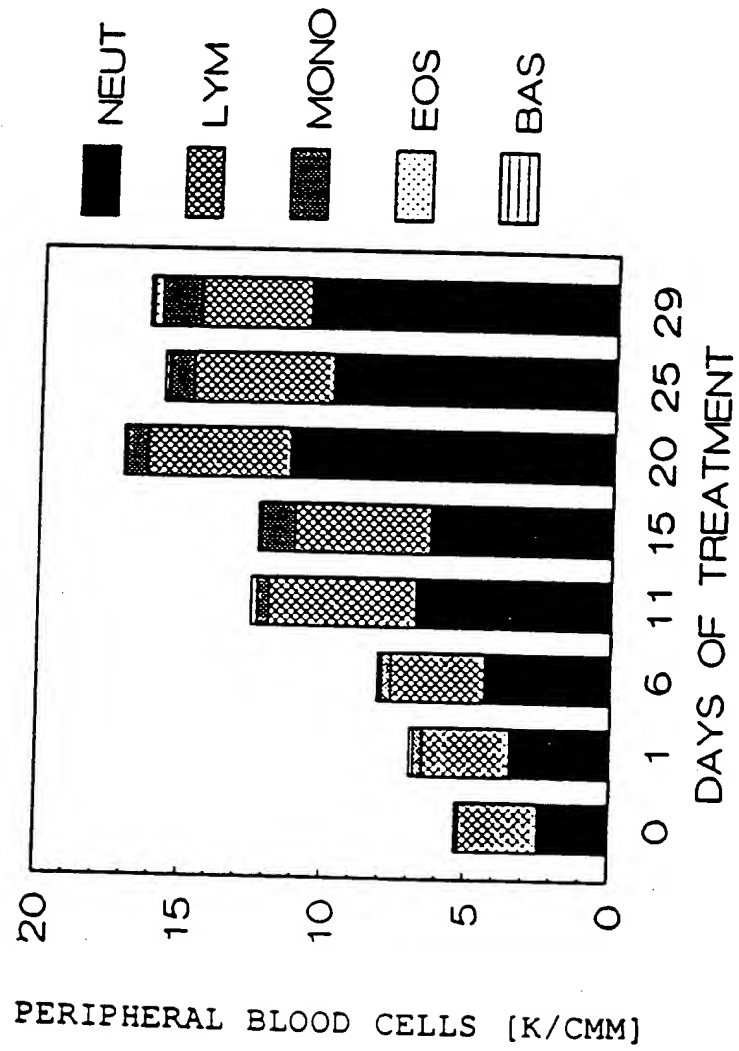


FIG.30A

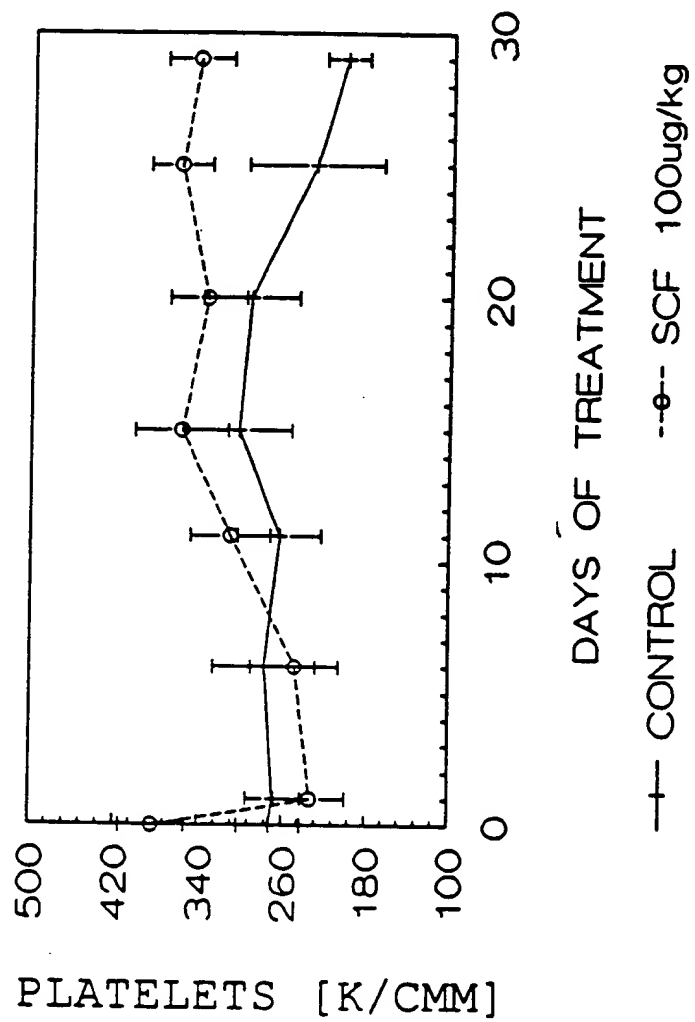


FIG. 30B

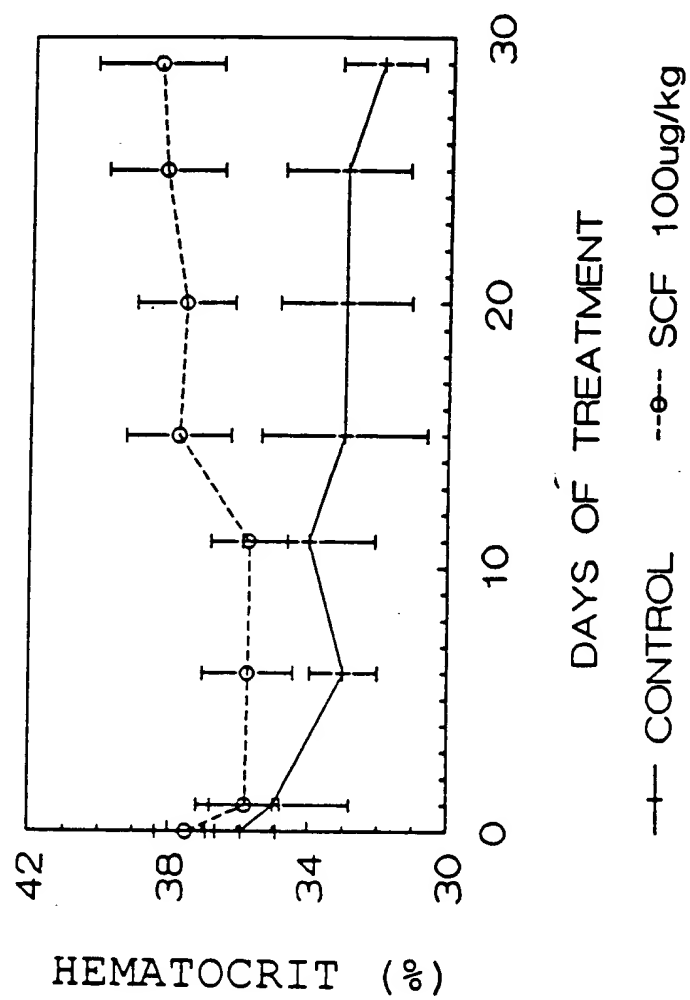


FIG. 31A

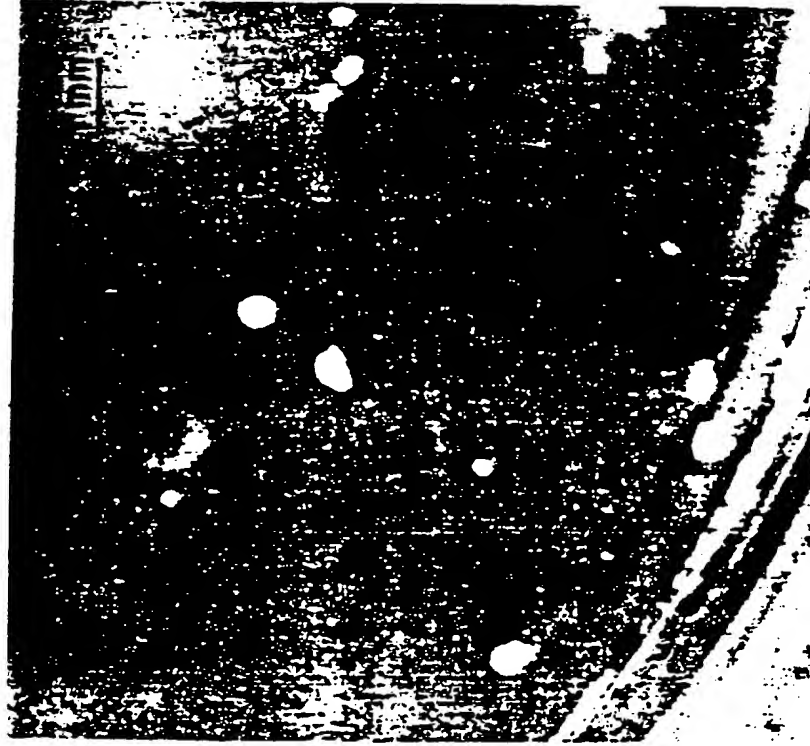
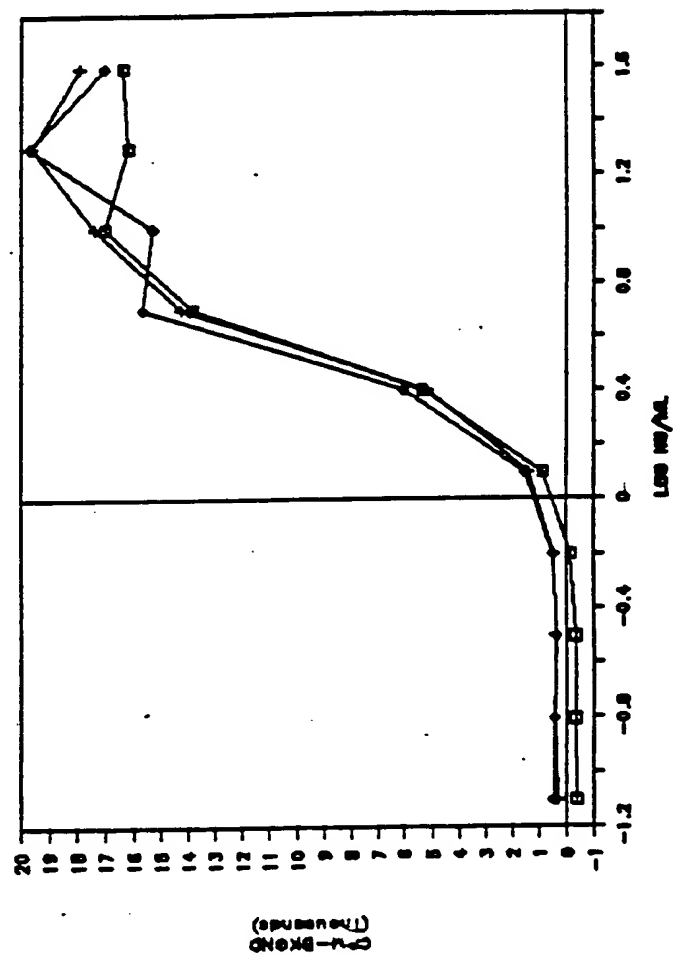


FIG. 31B



FIG. 31C

SCF4 SMP4



Sephacose Load

FIG. 32A

11 15 19 23 27 31 35 37



97.4 —

66.2 —

42.7 —

31.1 —

21.5 —

14.4 —

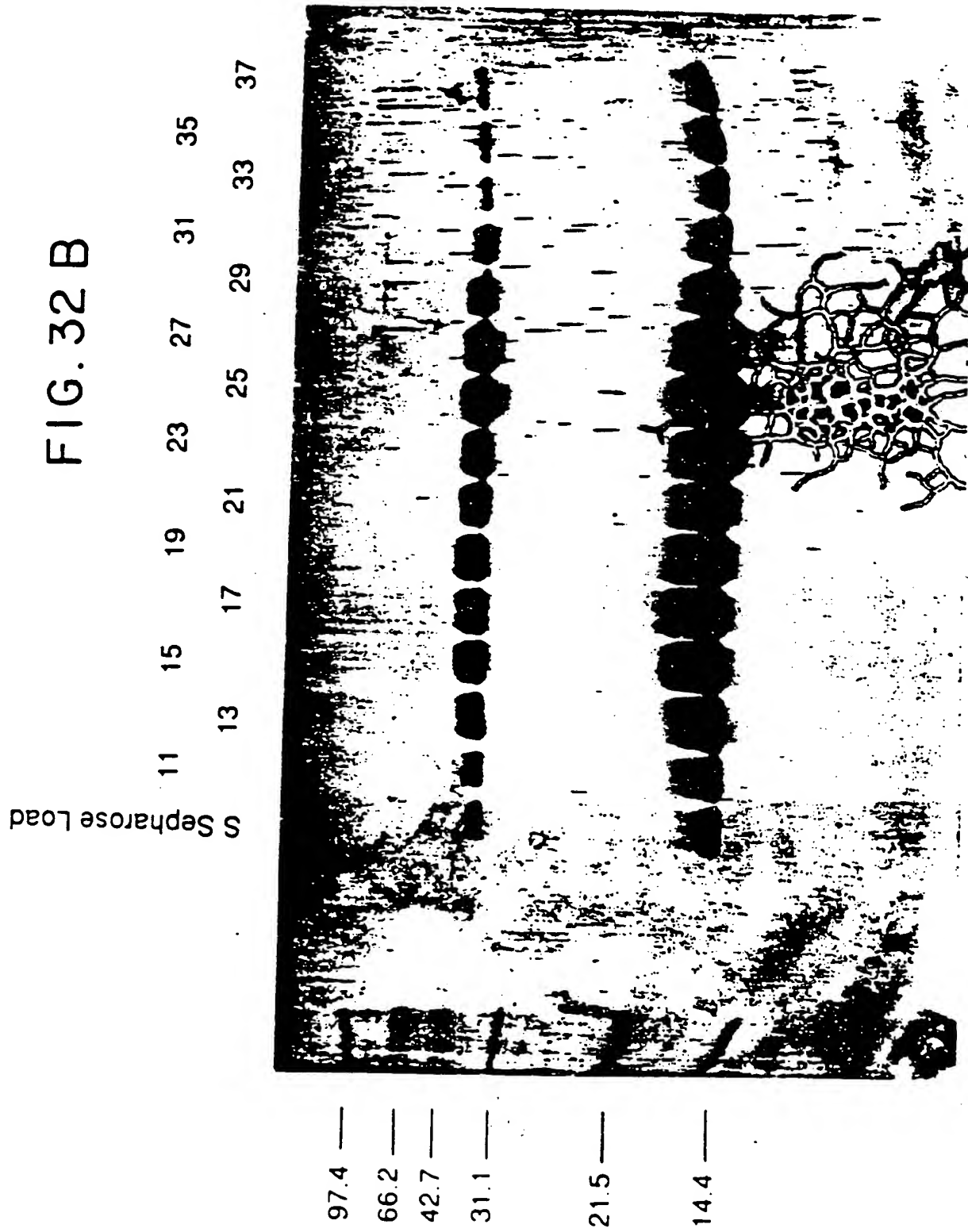


FIG. 33

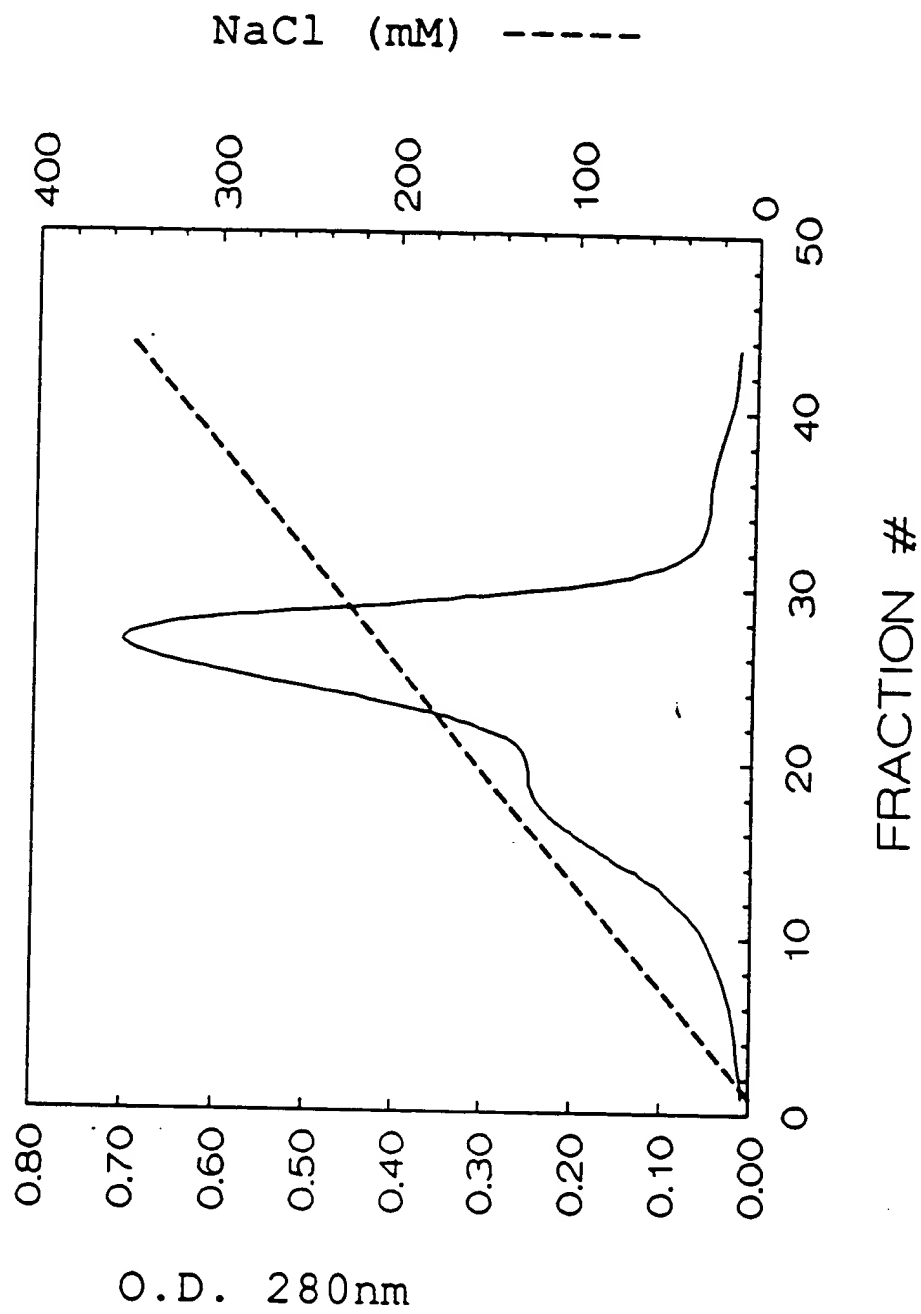
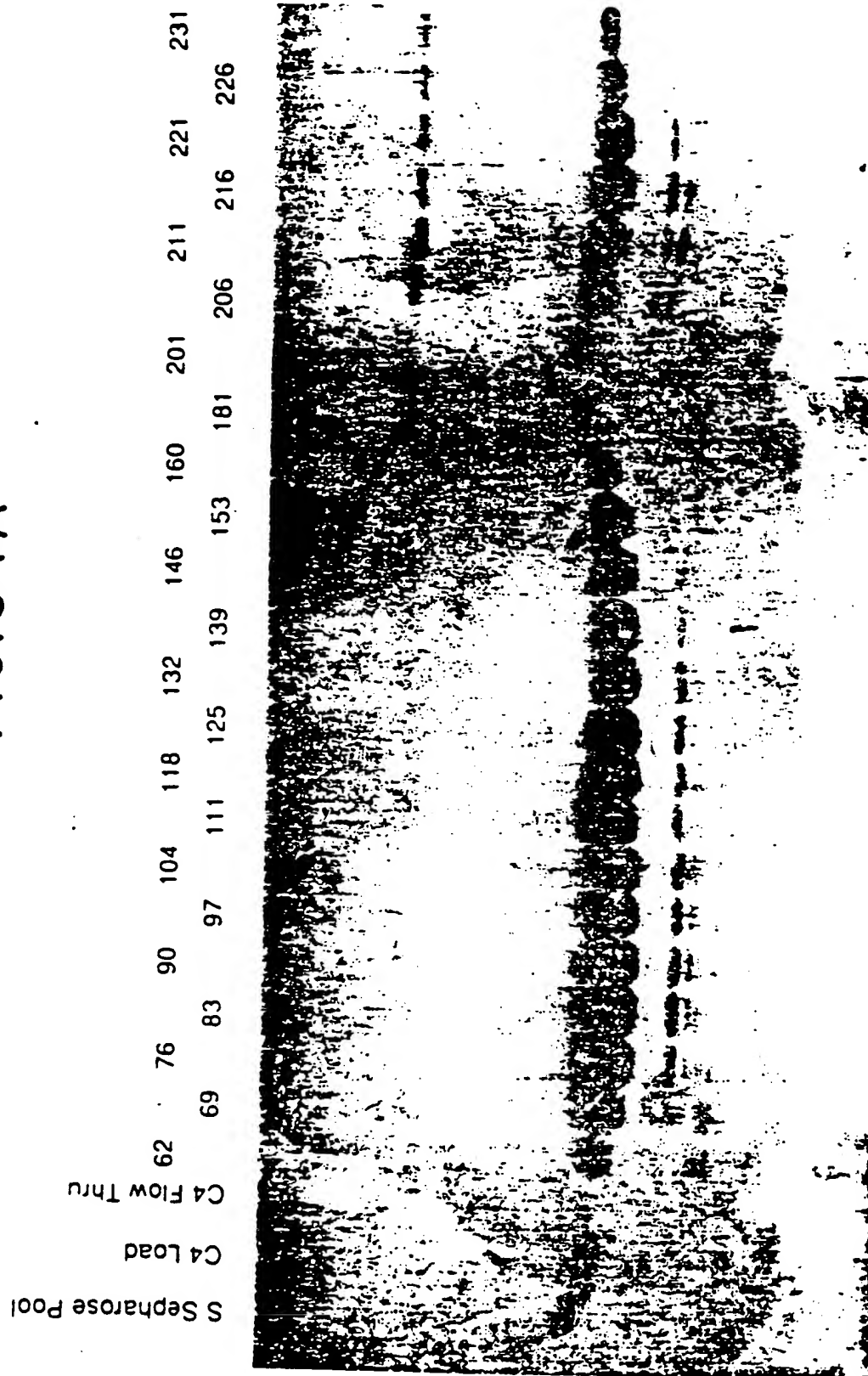


FIG. 34A



97.4

66.2

42.7

31.1

21.5

14.4

FIG. 34B

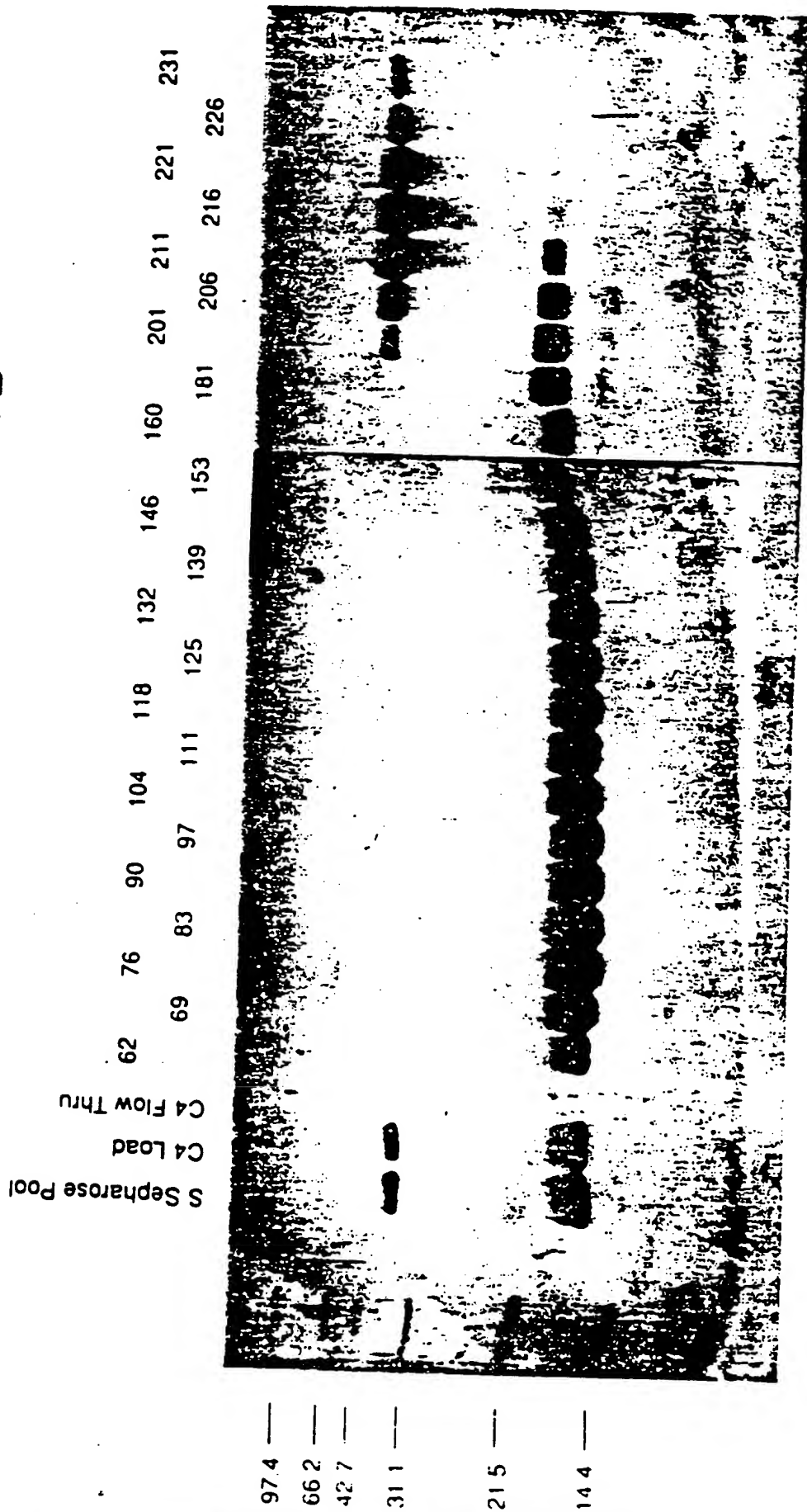


FIG. 35

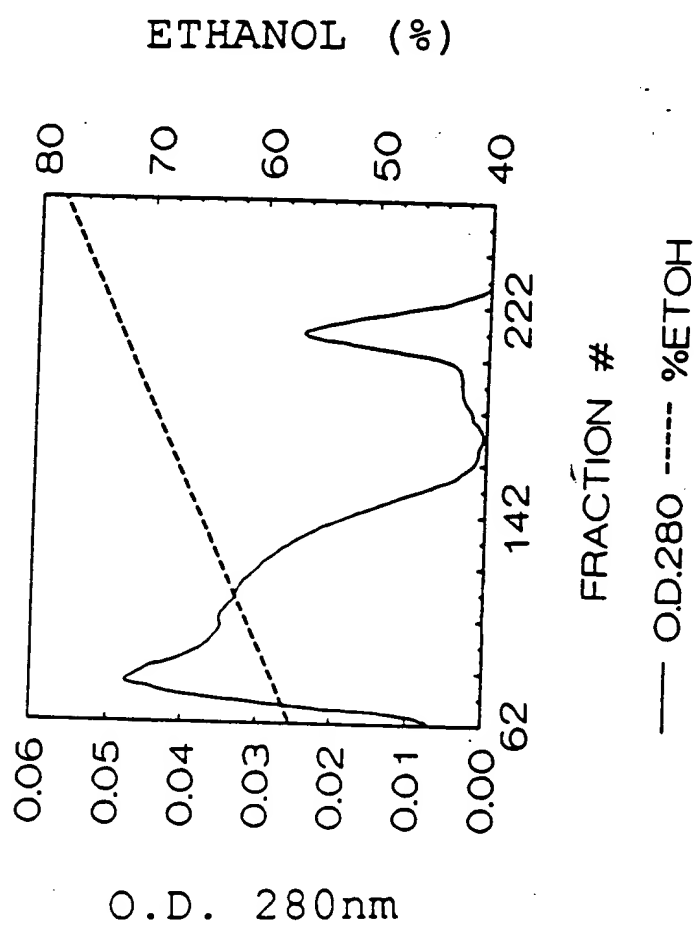


FIG. 36

MC/9 CPM ($\times 10^{-3}$)

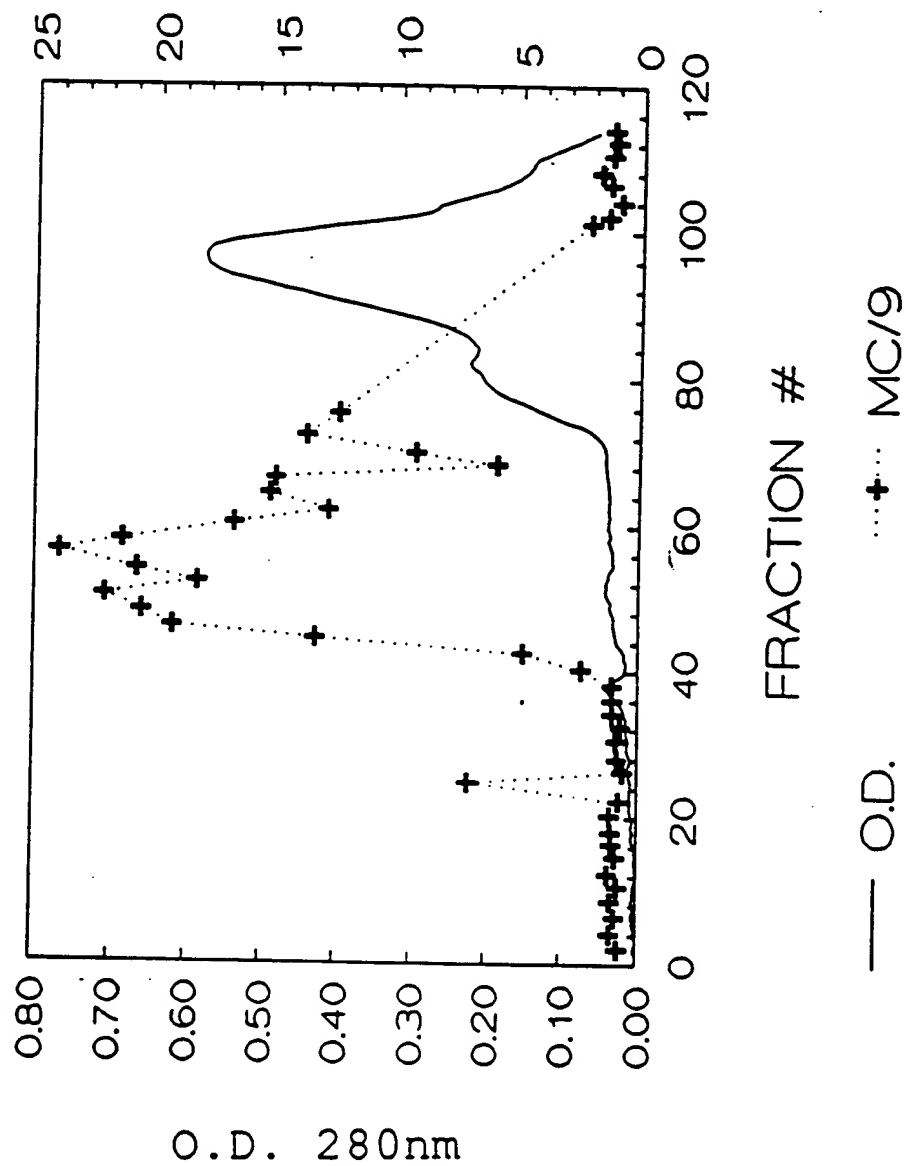
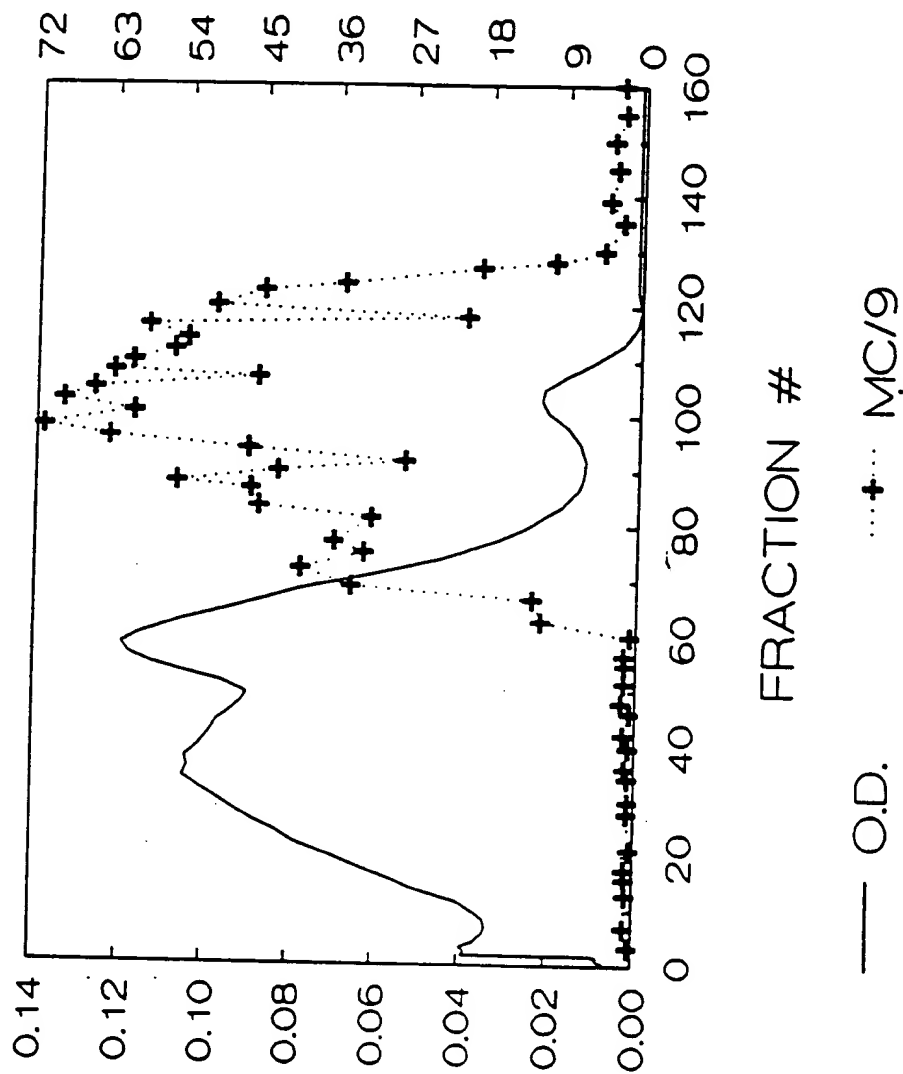


FIG. 37

MC/9 CPM ($\times 10^{-3}$)



O.D. 280nm ($\times 10^1$)

1 2 3 4 5 6 7 8 9

Q

FIG. 40A

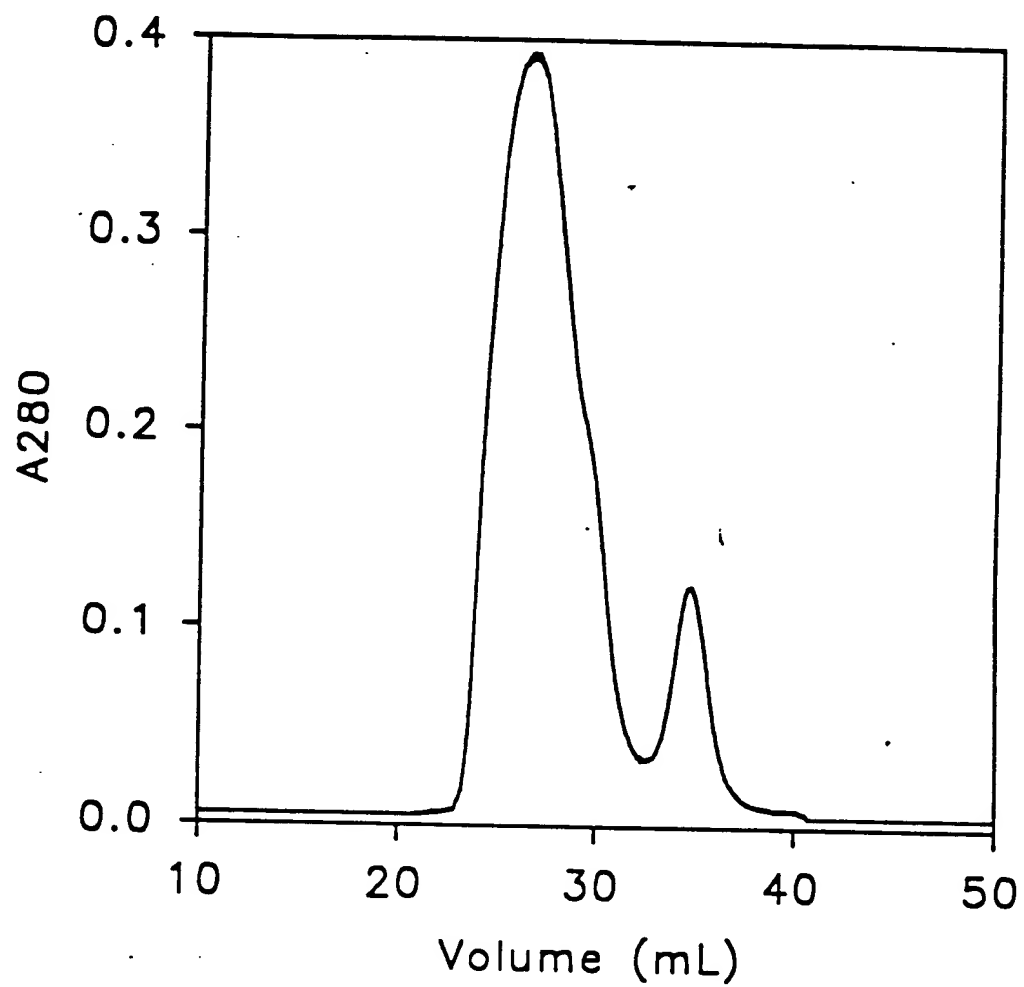


FIG. 40B

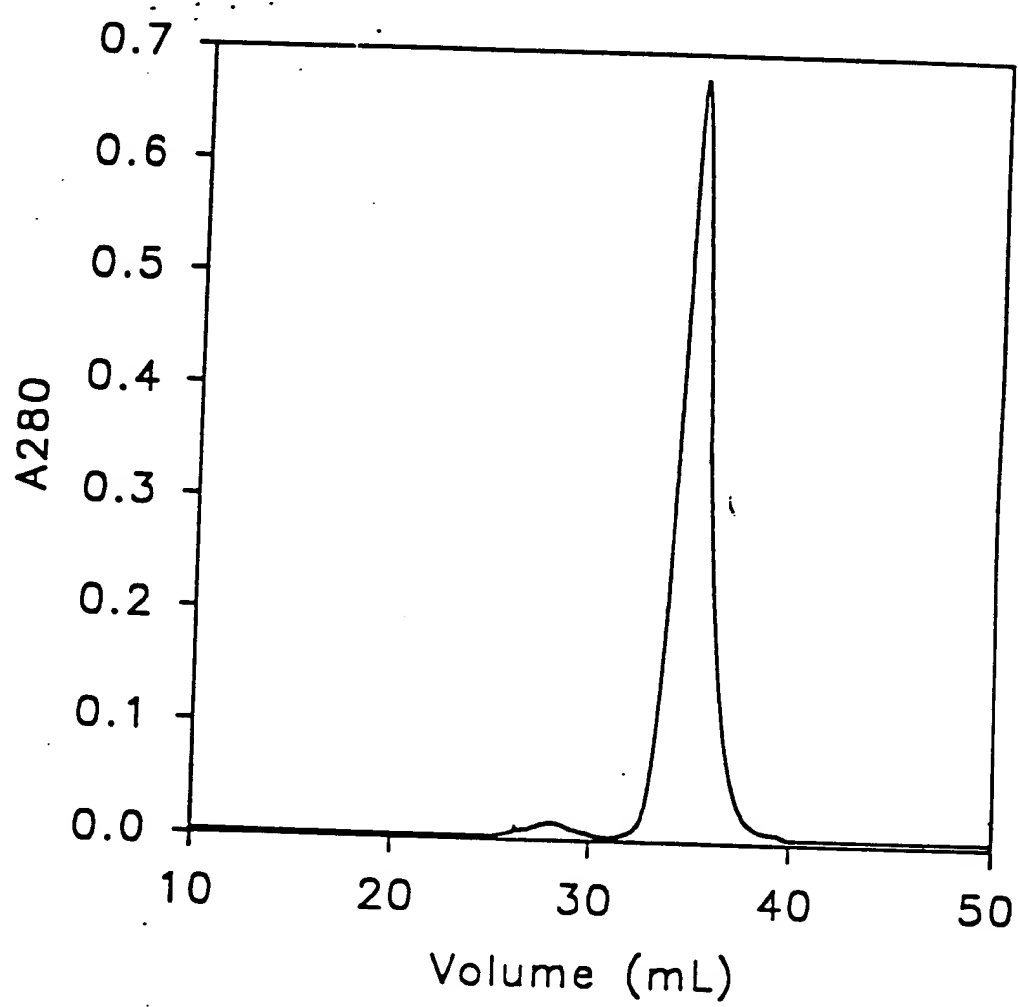


FIG. 41

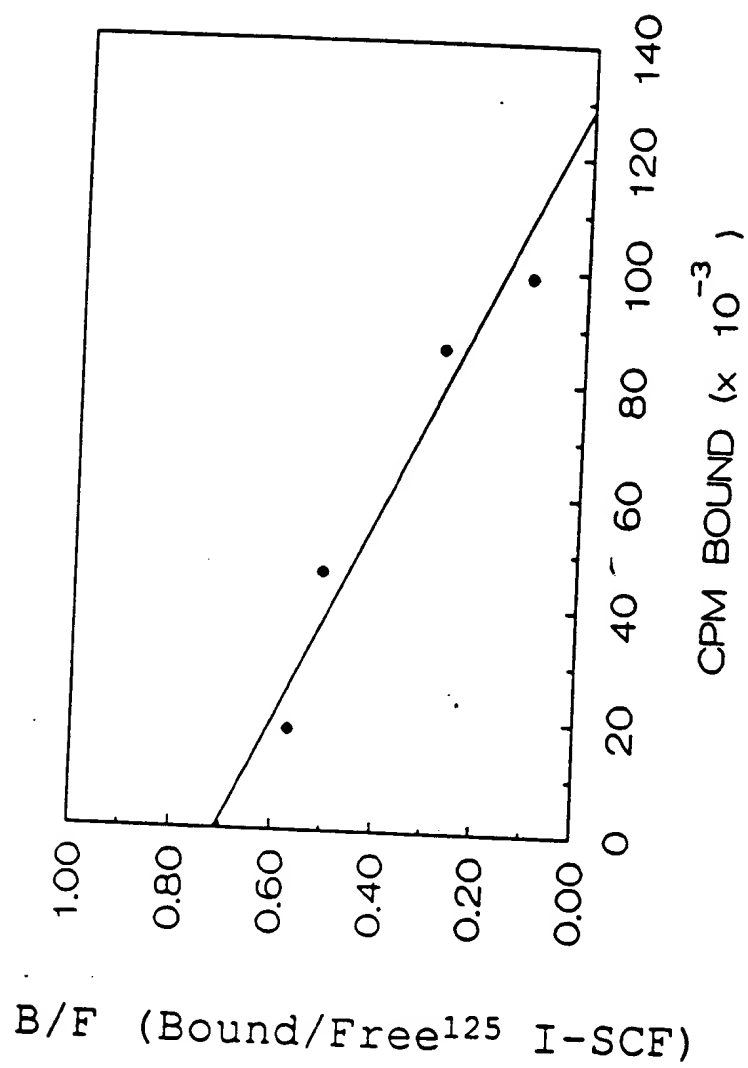


FIG. 42A

CCGCCCTCGCGCCGAGACTAGAACGCTGCGGGGAAGCAGGACAGTGGAGAGGGCGCTGCGC 61

TCGGGGCTACCCCAATGCGTGGACTATCTGCCCGCGCTGTTCGTGCAATATGCTGGAGCTCCA 122

GAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCCTTTCCTT 183

-25

-20

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG 228

-10

1

Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG 273

10

Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA 318

20

30

Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG 363

40

Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA 408

50

60

Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT 453

FIG. 42B

Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val	80
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG	498
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser	90
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT	543
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe	110
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT	588
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala	120
ACT CCT GAA GAA TTC TTT TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC	633
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val	140
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT	678
Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr	150
TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA	723

FIG. 42C

Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	Leu	Arg	Asn	170
AAA	CCA	TTT	ATG	TTA	CCC	CCT	GTT	GCA	GCC	AGC	TCC	CTT	AGG	AAT	768
Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Lys	Asn	Pro	Pro	Gly	Asp	180
GAC	AGC	AGT	AGC	AGT	AAT	AGG	AAG	GCC	AAA	AAT	CCC	CCT	GGA	GAC	813
Ser	Ser	Leu	His	Trp	Ala	Ala	Met	Ala	Leu	Pro	Ala	Leu	Phe	Ser	200
TCC	AGC	CTA	CAC	TGG	GCA	GCC	ATG	GCA	TTG	CCA	GCA	TTG	TTT	TCT	858
Leu	Ile	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Arg	210
CTT	ATA	ATT	GGC	TTT	GCT	TTT	GGA	GCC	TTA	TAC	TGG	AAG	AAG	AGA	903
Gln	Pro	Ser	Leu	Thr	Arg	Ala	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	230
CAG	CCA	AGT	CTT	ACA	AGG	GCA	GTT	GAA	AAT	ATA	CAA	ATT	AAT	GAA	948
Glu	Asp	Asn	Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	240
GAG	GAT	AAT	GAG	ATA	AGT	ATG	TTG	CAA	GAG	AAA	GAG	AGA	GAG	TTT	993
Gln	Glu	Val	End												248
CAA	GAA	GTG	TAA												
TTGTGGCTTGATCAACACTGTTACTTTCGTACATTGGC 1044															

FIG. 42D

TGGTAACAGTTTCATGTTTGCTTCATAAATGAAGCAGCCTTTAAACAAATTCATATCTCTGTC 1104
TGGAGTGACAGACCATCTTTATCTGTTCTTGCTACCCATGACTTTATATGGATGATTC 1164
AGAAATTGGAAACAGAAATGTTTACTGTGAAACTGGCACTGAATTAATCATCTATAAAGAA 1224
GAACTTGCCATGGAGCAGGACTCTATTTTAAGGACTGCCGGGACTTGGGTCTCATTTAGAAC 1284
TTGCAGCTGATGTTGGAAGAGAAAGCACGTGTCTCAGACTGCATGTACCAATTTGCATGGC 1344
TCCAGAAAATGCTCTAAATGCTGAAAAAACACCTAGCTTTATTCTTCAGATACAAACTGCAG 1404

FIG. 43

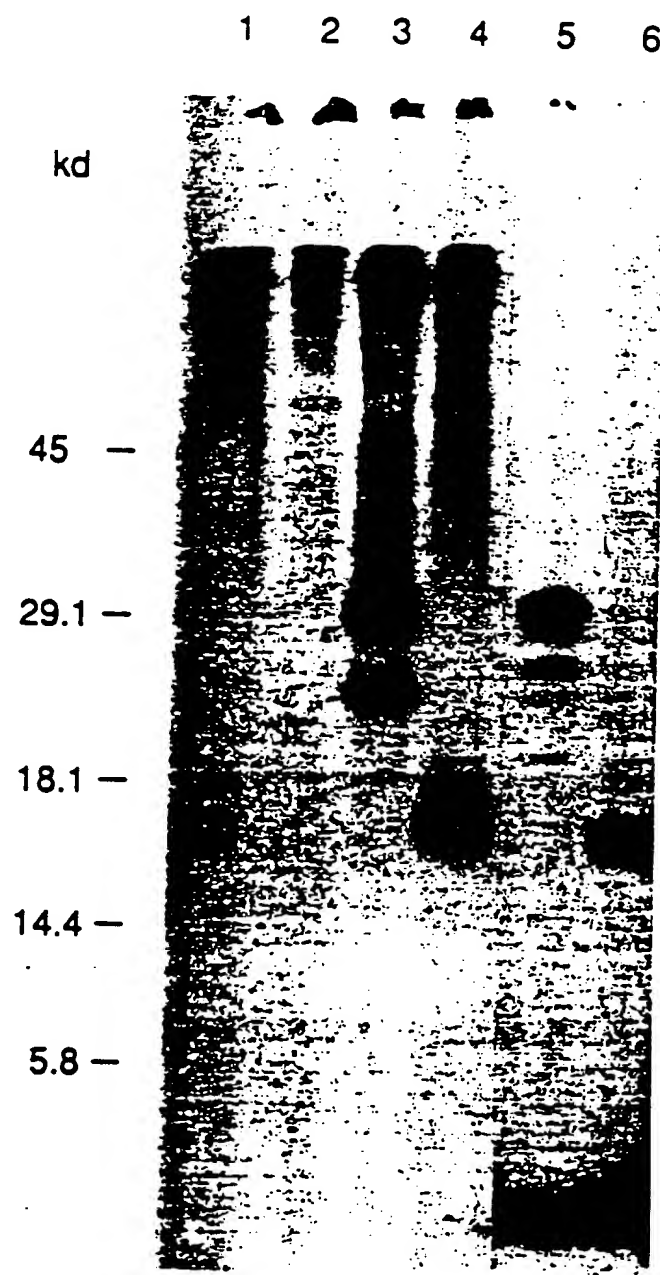


FIG. 44A

	AGCAGGGACAGTGGAGAGGGCGCTGCGCTC	30
GGGCTACCCAATGCGTGGACTATCTGCCCGCGCTGTTTCGTGCAATATGCTGGAGCTCCAG		90
AACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCCTTTCCTT		150
-25		
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln		
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG		195
-20		
-10		
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg	1	
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG		240
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala	20	
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA		285
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly	30	
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG		330
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val	50	
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA		375
40		

Gln	Leu	Ser	Asp	Ser	Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	
CAA	TTC	TCA	GAC	AGC	TTG	ACT	GAT	CTT	CTG	GAC	AAG	TTT	TCA	AAT	
								70							420
Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	
ATT	TCT	GAA	GGC	TTG	AGT	AAT	TAT	TCC	ATC	ATA	GAC	AAA	CTT	GTG	
									90						465
Asn	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	
AAT	ATA	GTG	GAT	GAC	CTT	GTG	GAG	TGC	GTG	AAA	GAA	AAC	TCA	TCT	
									100						510
Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	Ser	Pro	Glu	Pro	Arg	Leu	Phe	
AAG	GAT	CTA	AAA	AAA	TCA	TTC	AAG	AGC	CCA	GAA	CCC	AGG	CTC	TTT	
									120						555
Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	
ACT	CCT	GAA	GAA	TTC	TTT	AGA	ATT	TTT	AAT	AGA	TCC	ATT	GAT	GCC	
									130						600
Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	Ser	Asp	Cys	Val	Val	
TTC	AAG	GAC	TTT	GTA	GTG	GCA	TCT	GAA	ACT	AGT	GAT	TGT	GTG	GTT	
									150						645
Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Gly	Lys	Ala	Lys	Asn	Pro	Pro	
TCT	TCA	ACA	TTA	AGT	CCT	GAG	AAA	GGG	AAG	GCC	AAA	AAT	CCC	CCT	
															690

FIG. 44C

```

160      Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu      170
      GGA GAC TCC AGC CTA CAC CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG      735

180      Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys
      TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG      780

190      Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile      200
      AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT      825

210      Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Glu Glu Lys Glu Arg
      AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA      870

220      Glu Phe Gln Glu Val End
      GAG TTT CAA GAA GTG TAA      TTGTGGCTGTATCAACACTGTTACTTTCGTA      920
      CATGGCTGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAATTCATA      980
      TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTCTTGCTACCCATGACTTTATATG      1040
      ATGATTCAGAAATTGGAACAGAAATGTTTTACTGTGAAACTGGCACTGA      1088

```

FIG. 45

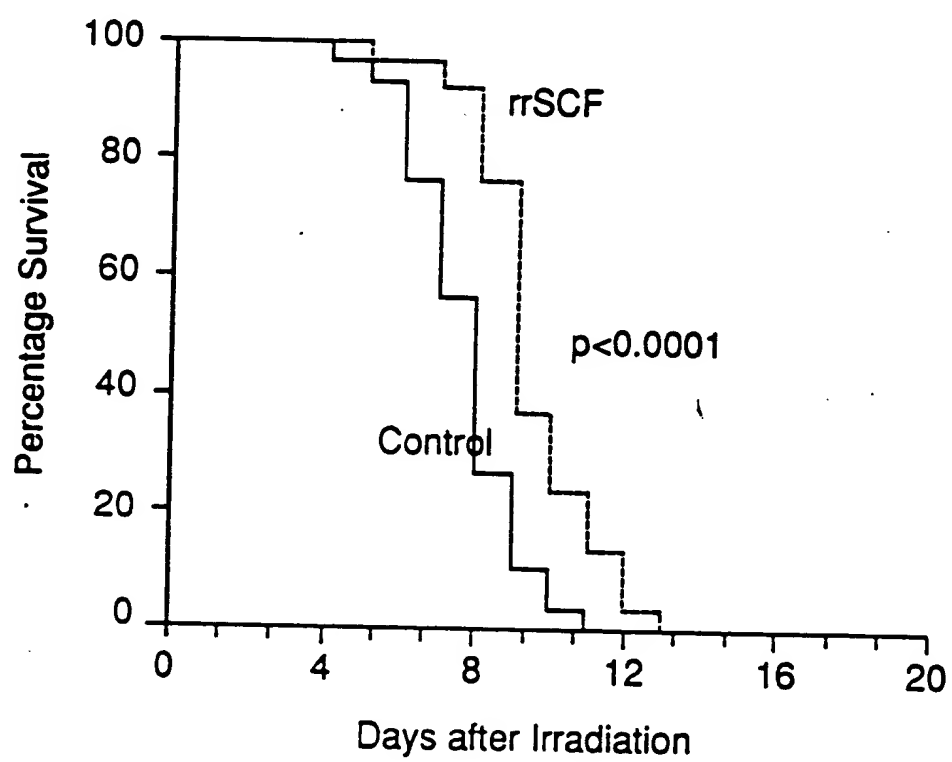
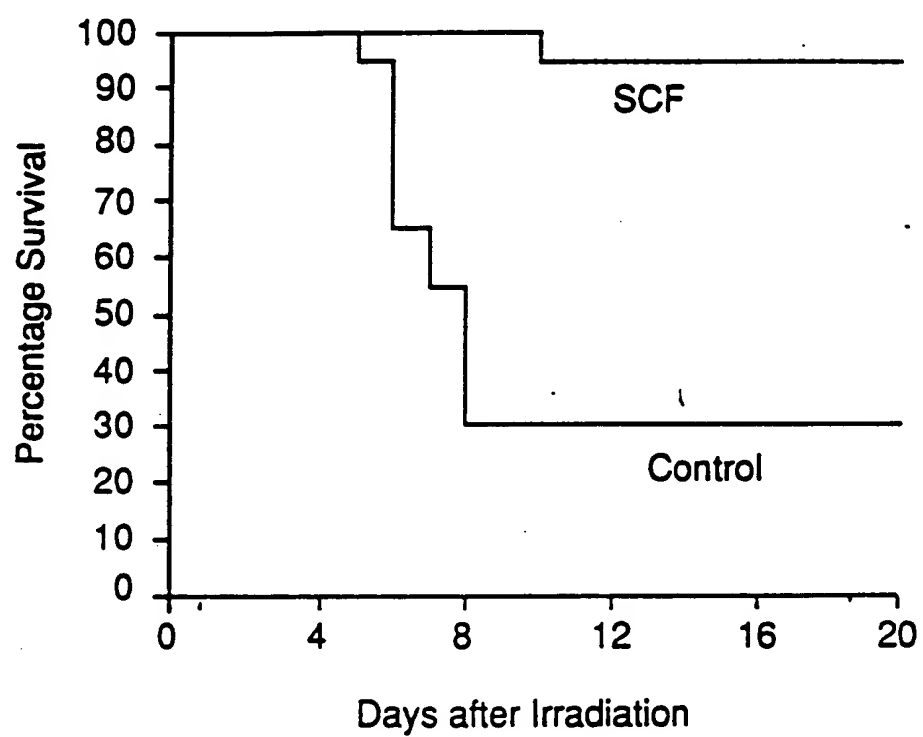


FIG. 46



850 RADS; 5% of femur transplanted

FIG. 47

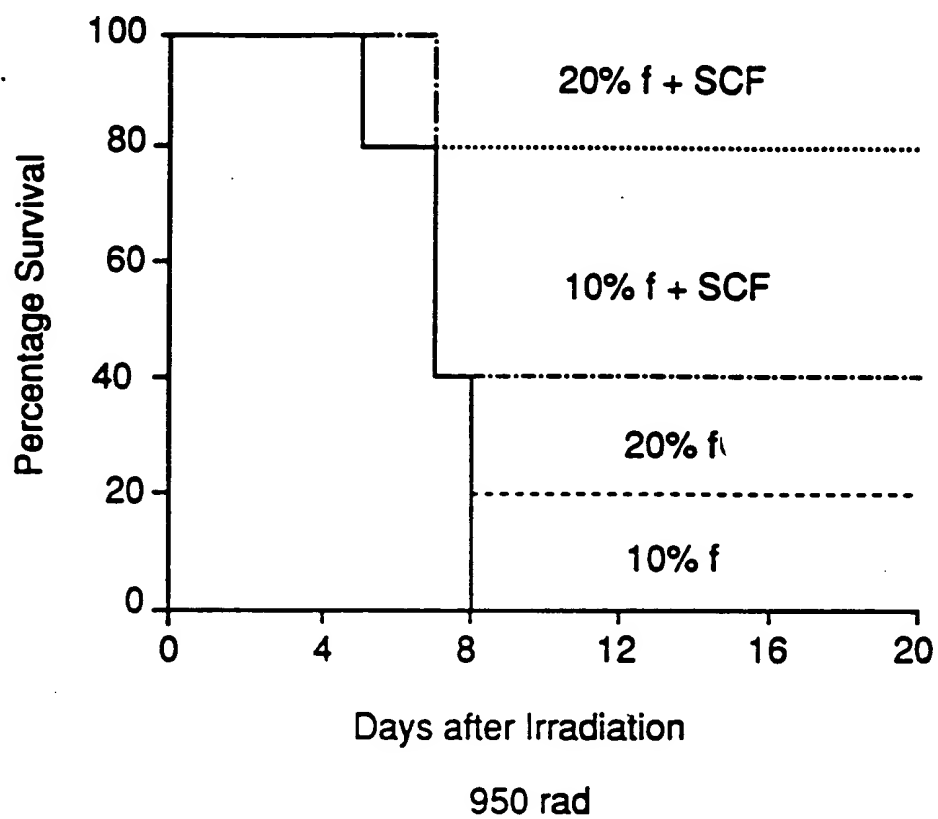


FIG. 48

SCF RADIOPROTECTION (1163 RAD)

Normal Female BDF1 mice, n=30

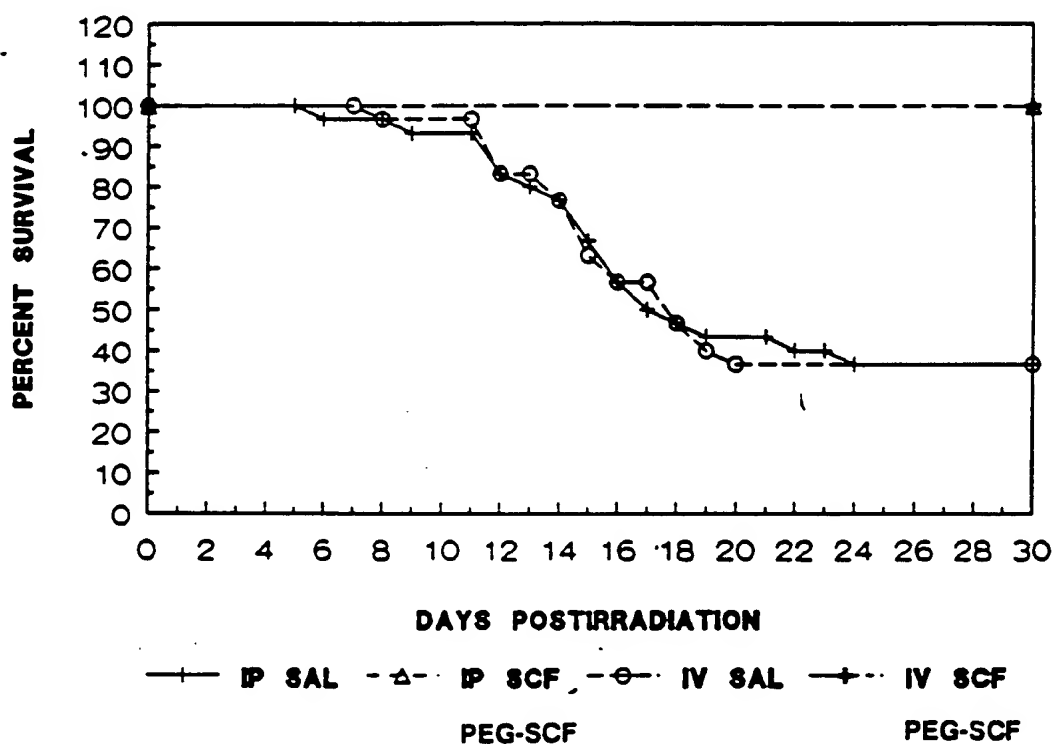


FIG. 49

SCF RADIOPROTECTION (1159 RAD)

Normal Female BDF1 mice

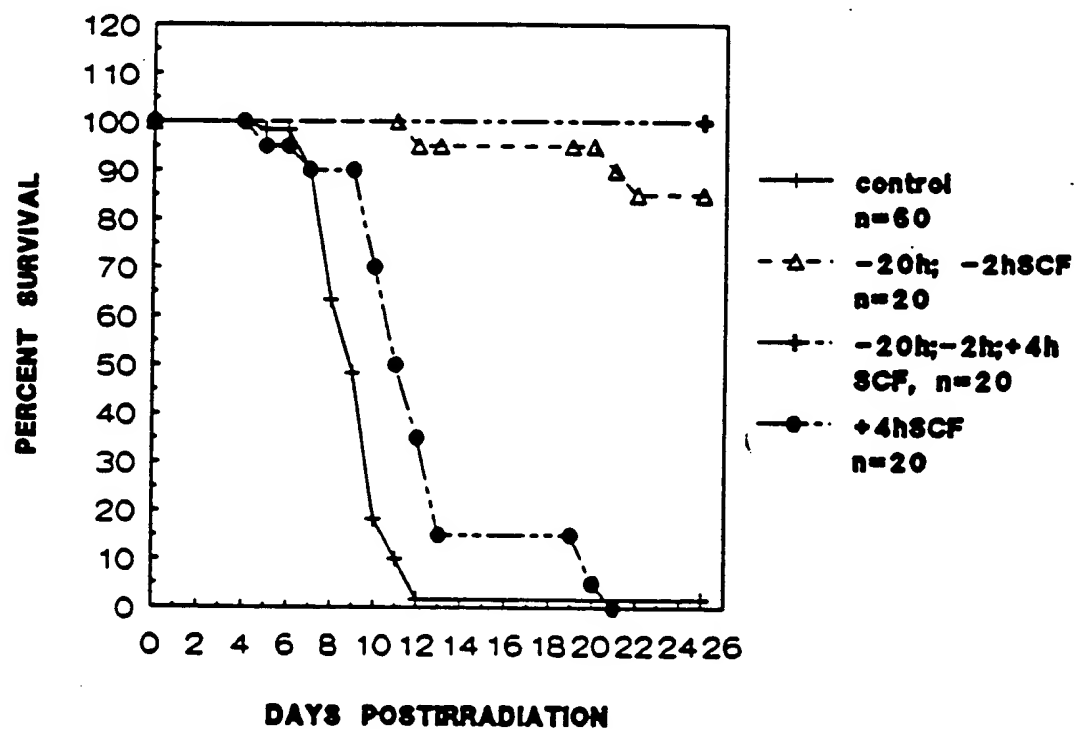


FIG. 50

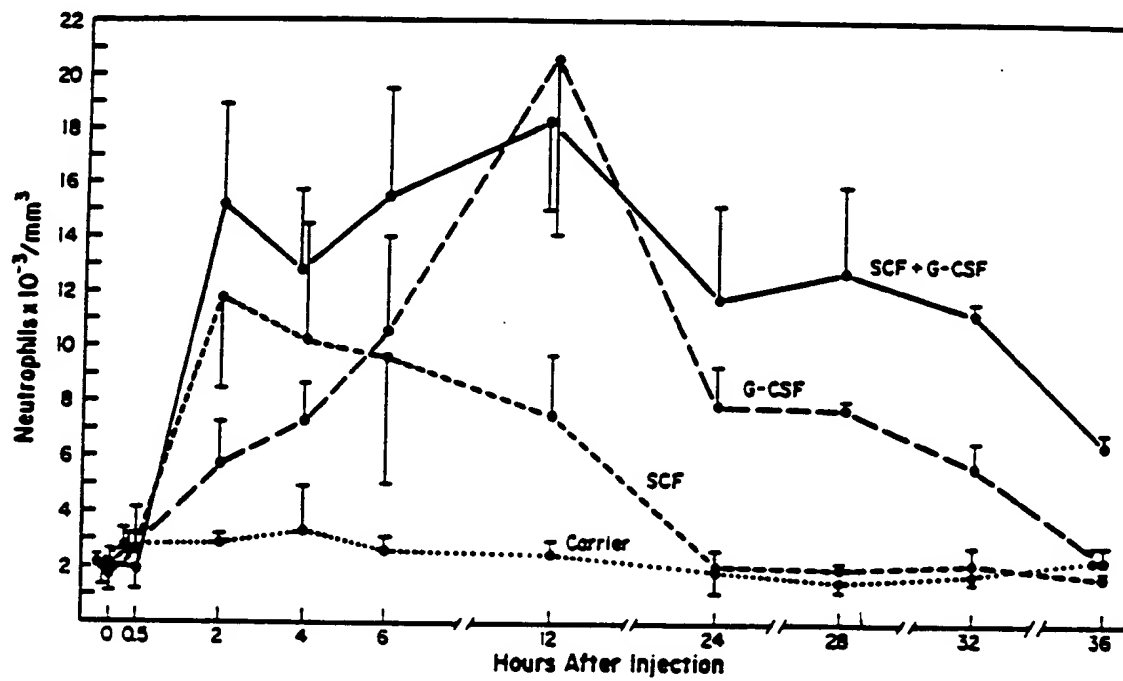


FIG. 51

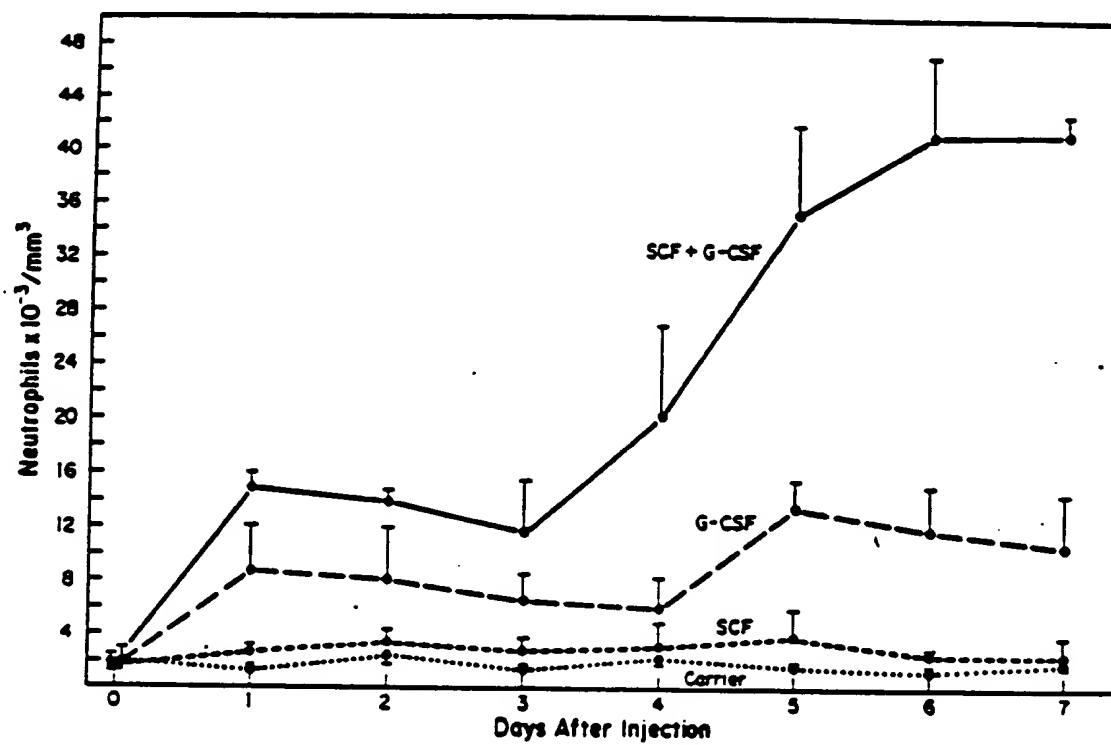


FIG. 52

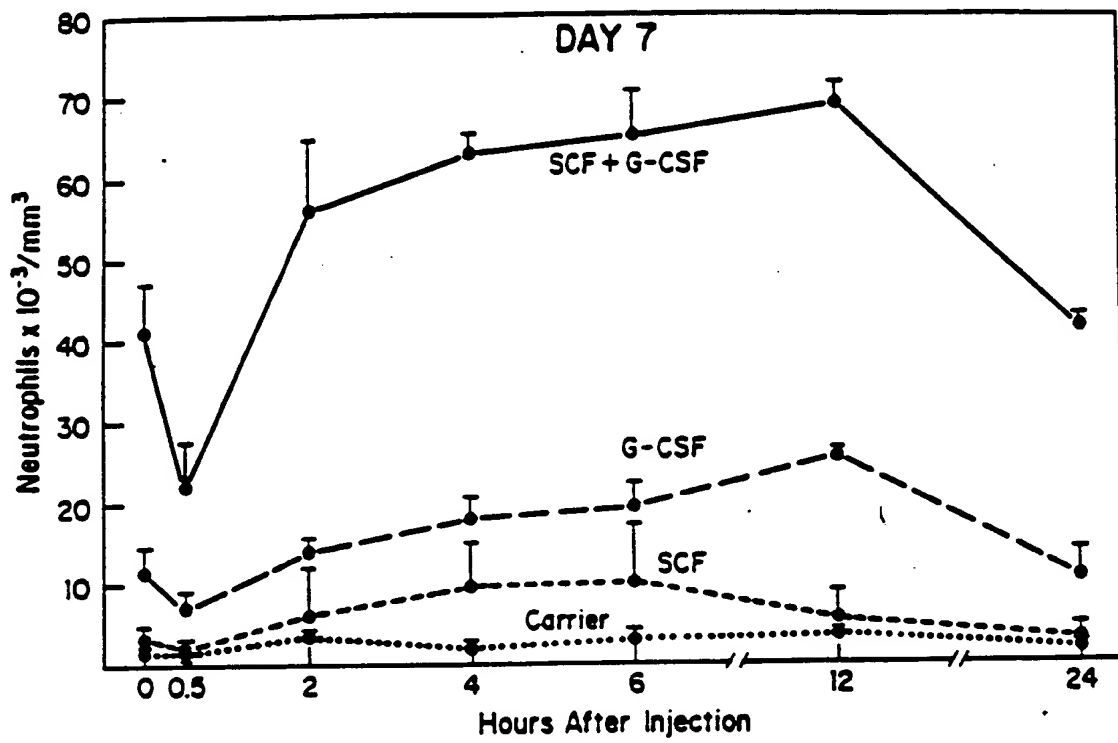


FIG. 53

in vivo Administration of SCF--Platelet Counts

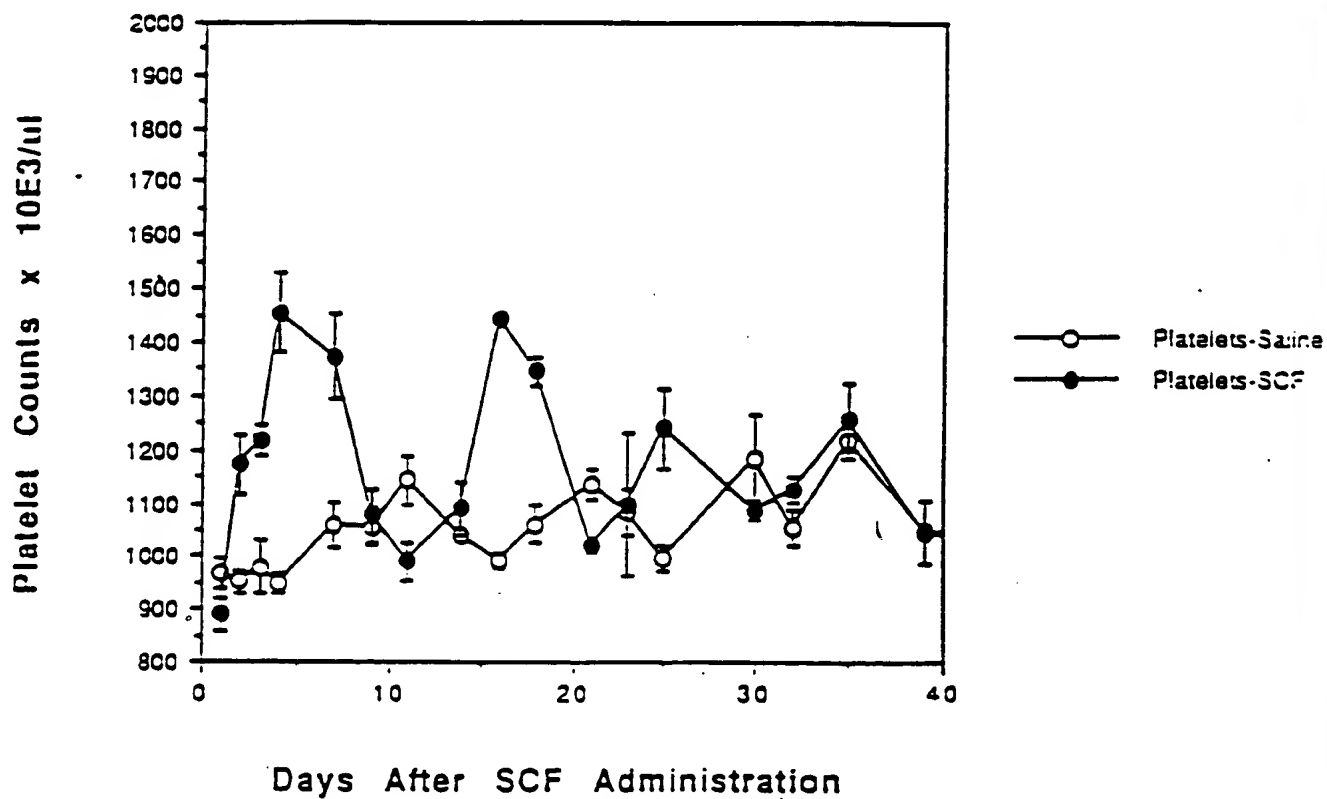


FIG. 54

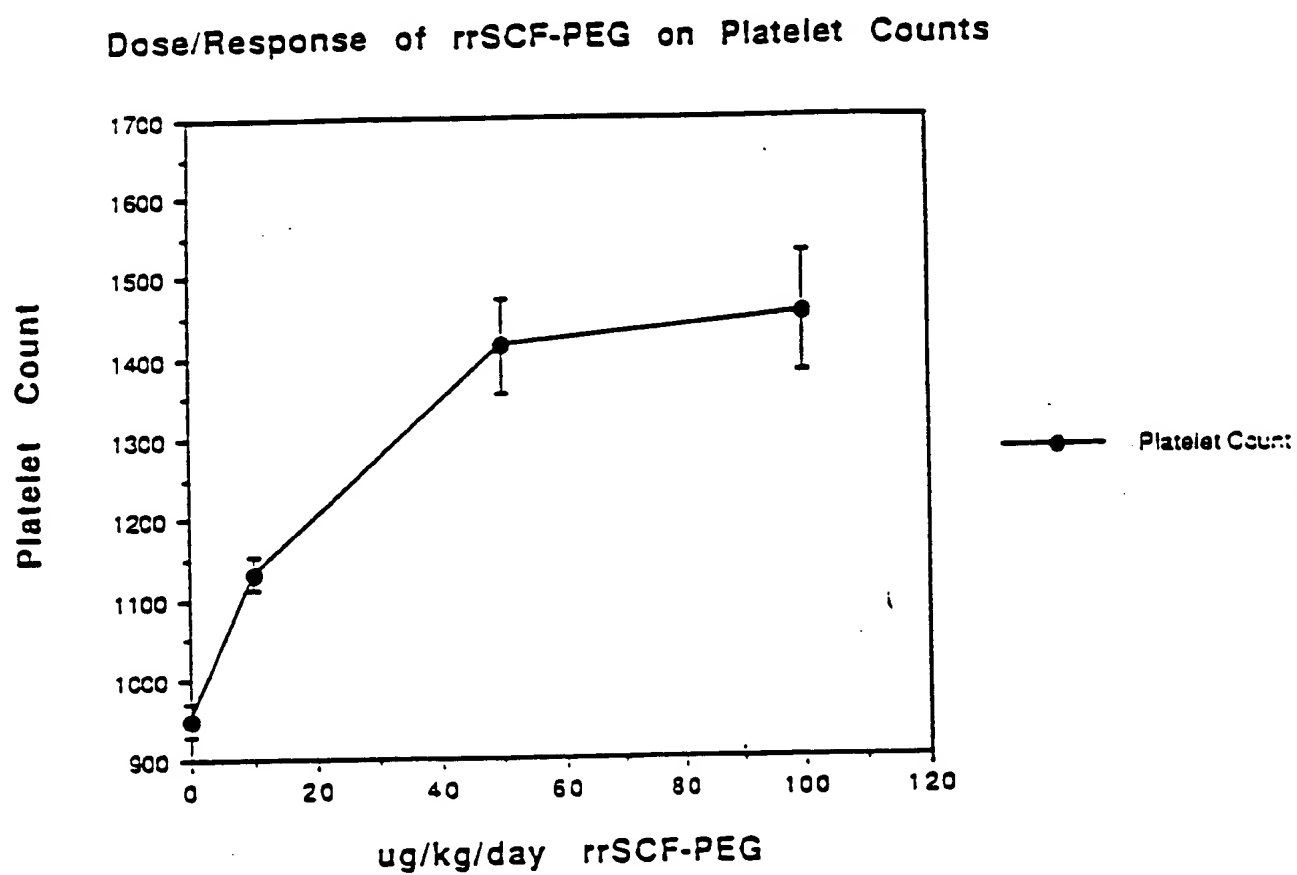


FIG. 55

Effect of 5-FU on platelet levels

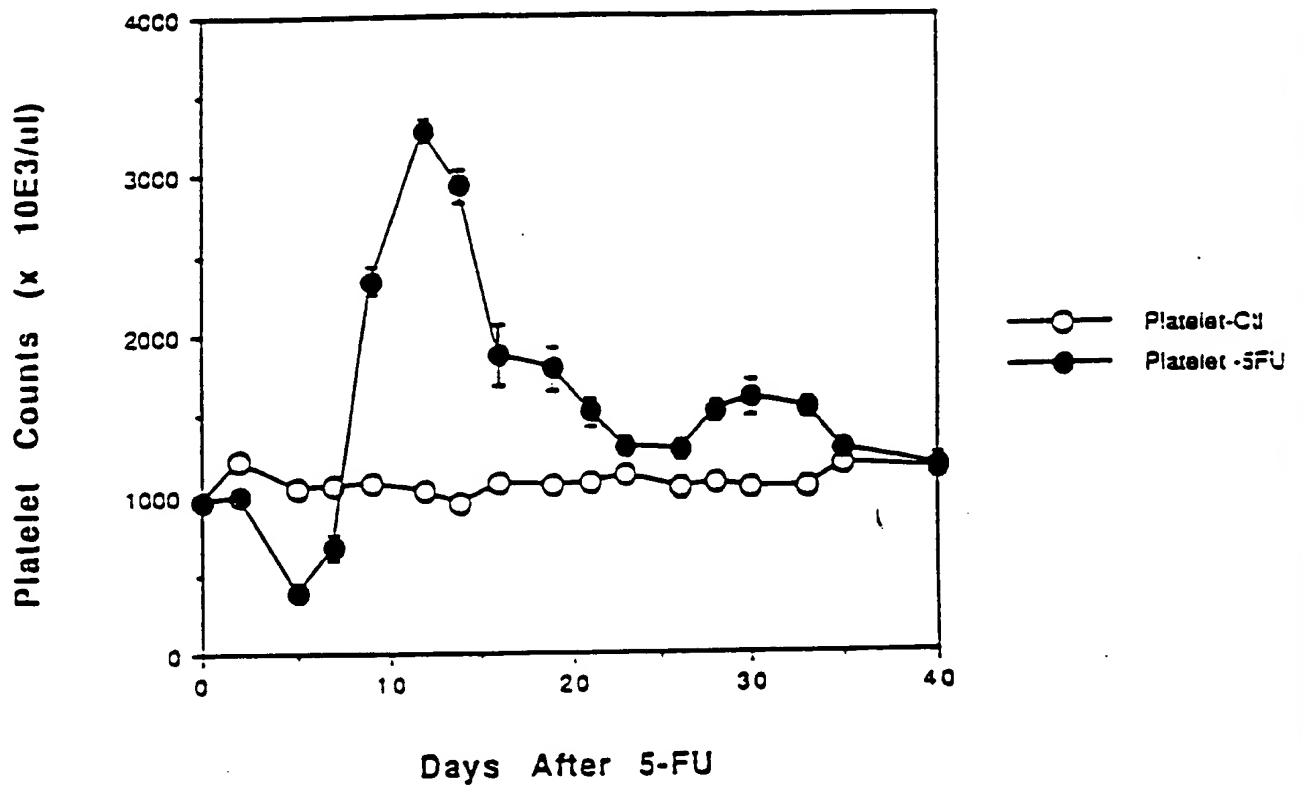
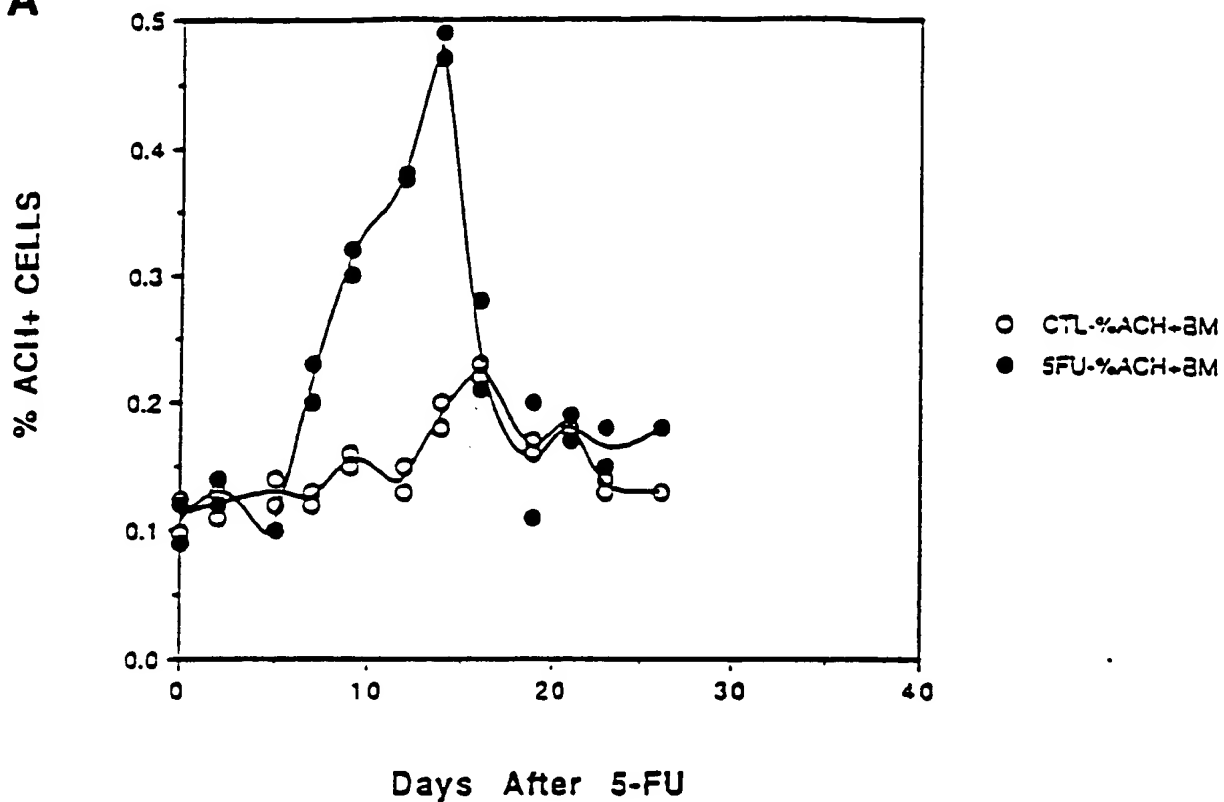


FIG. 56

5-FU Effect on ACH+ Cells in Marrow

A



5-FU Effect on ACH+ Cells in Spleen

B

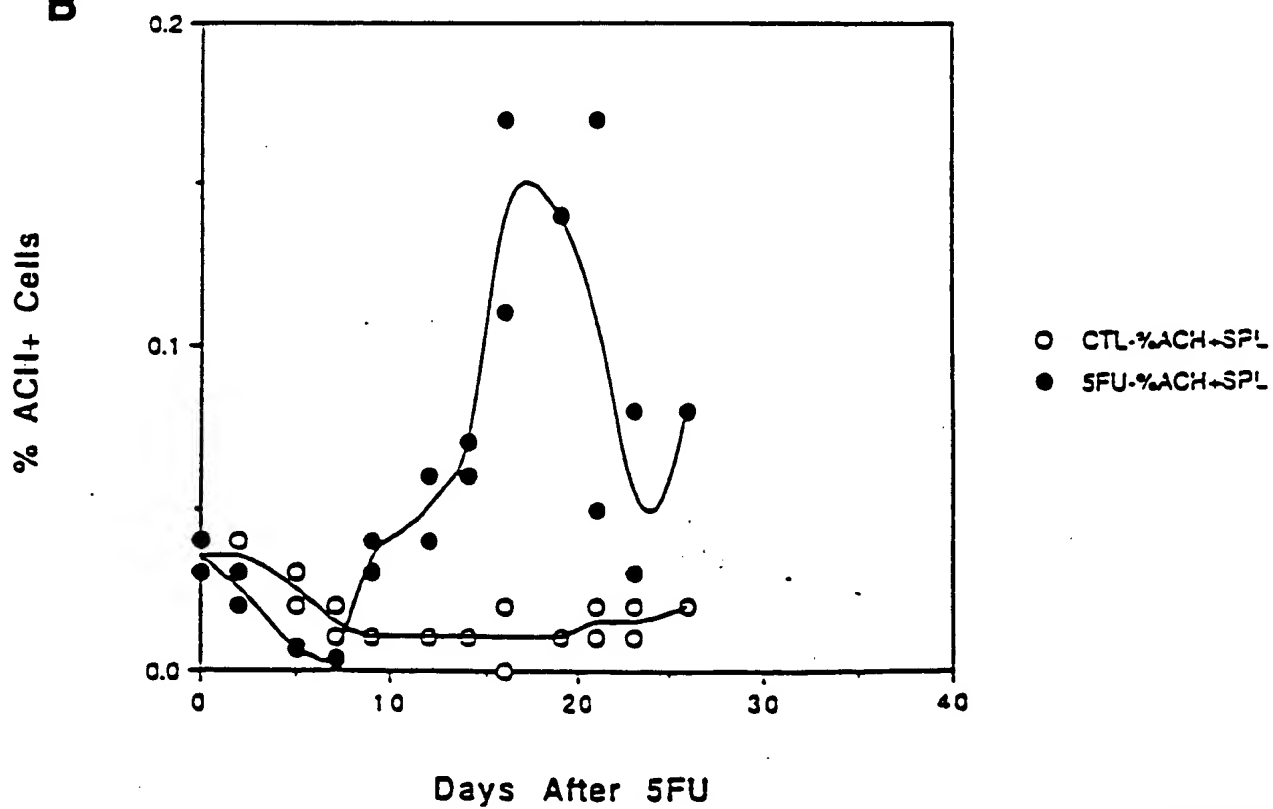


FIG. 57

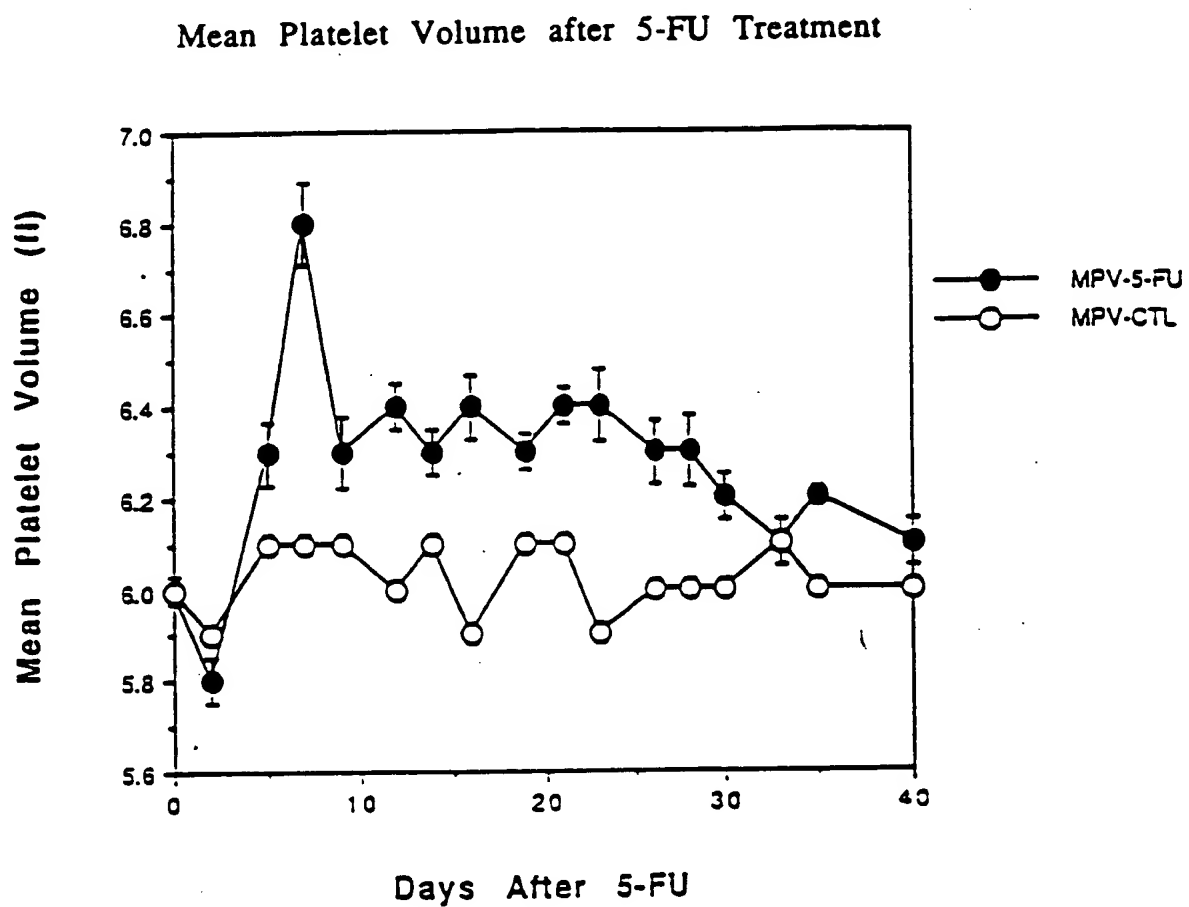


FIG. 58

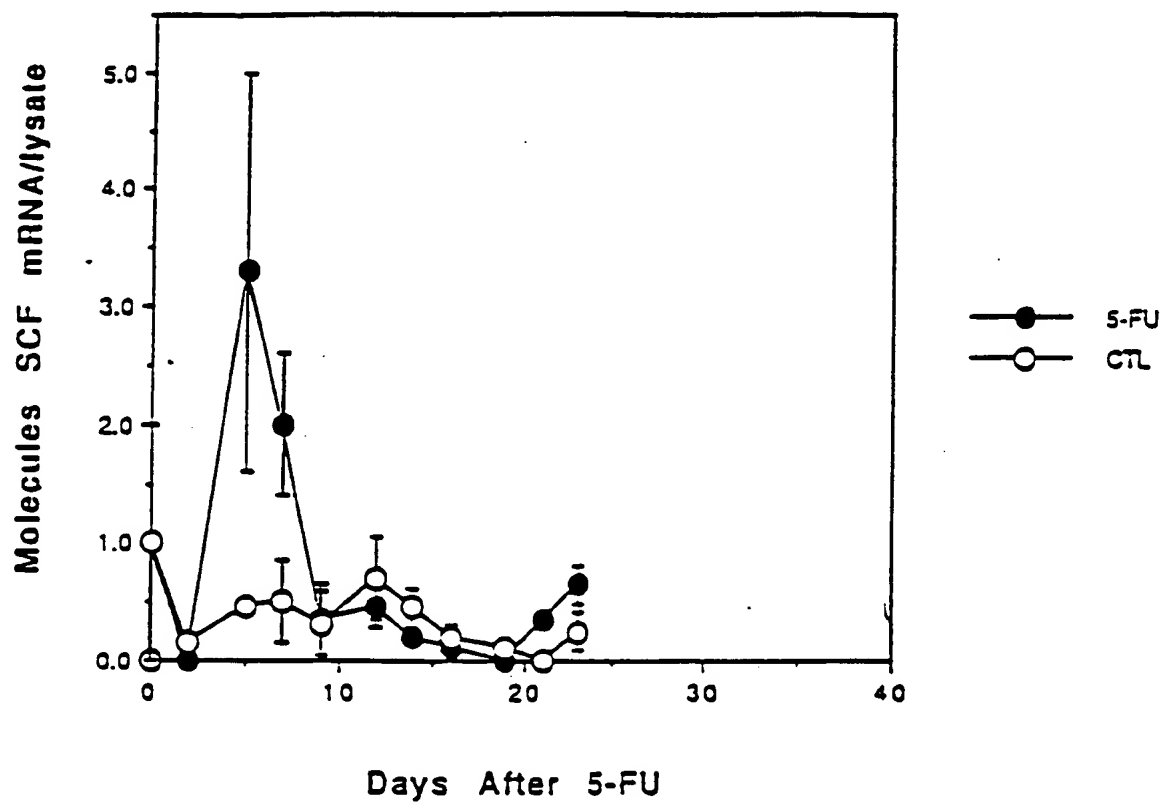


FIG. 59

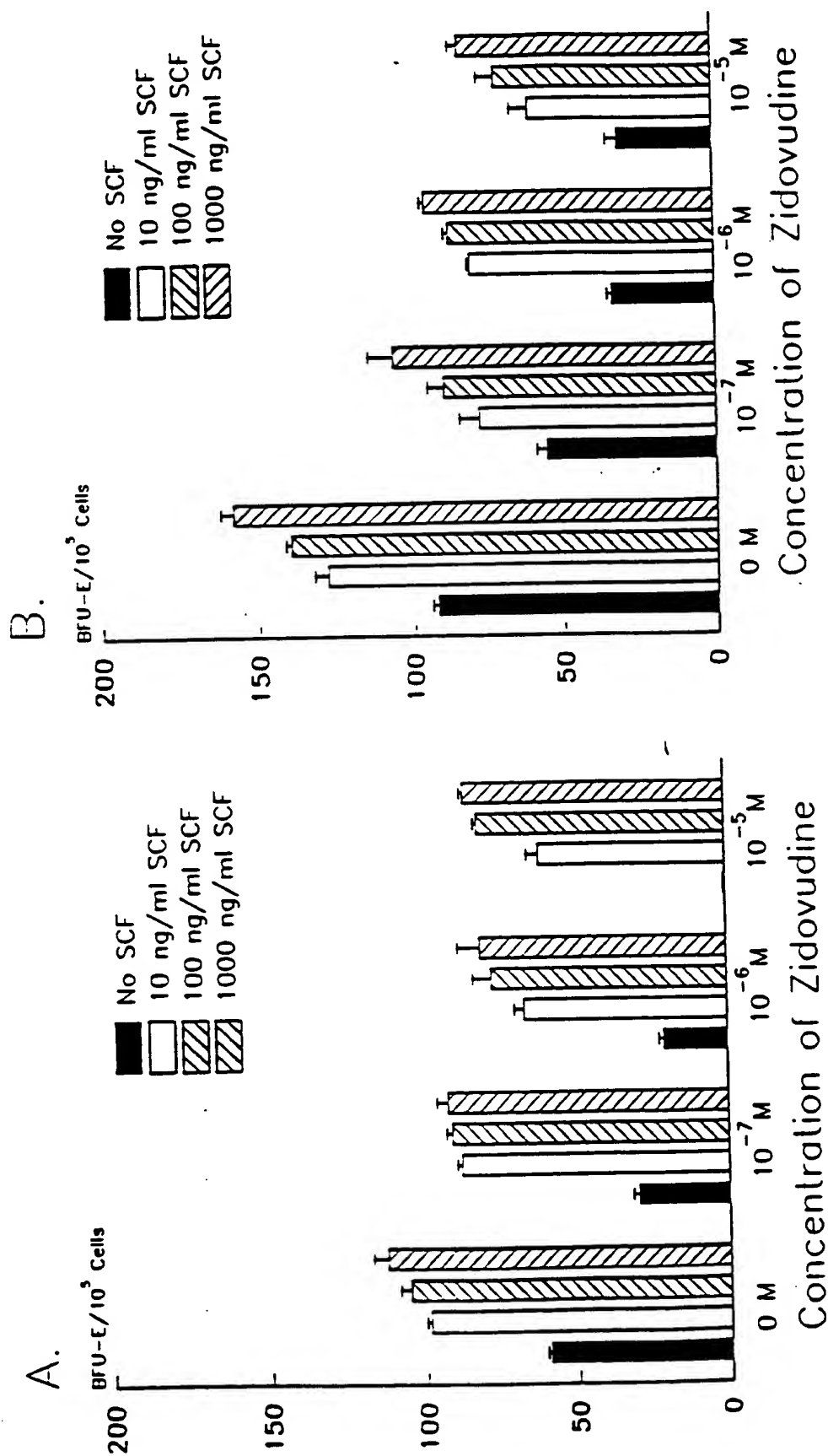


FIG. 60

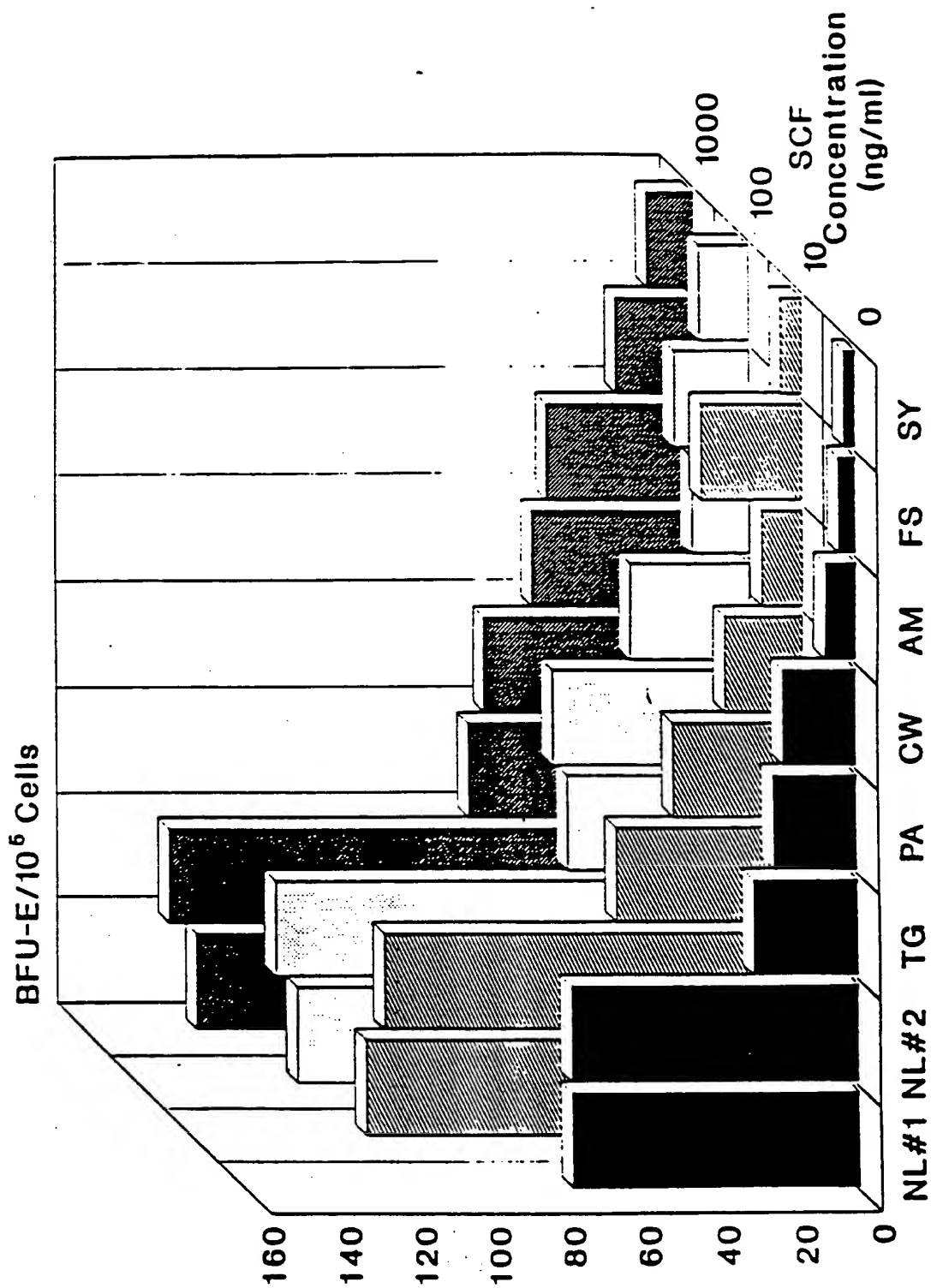


FIG: 61

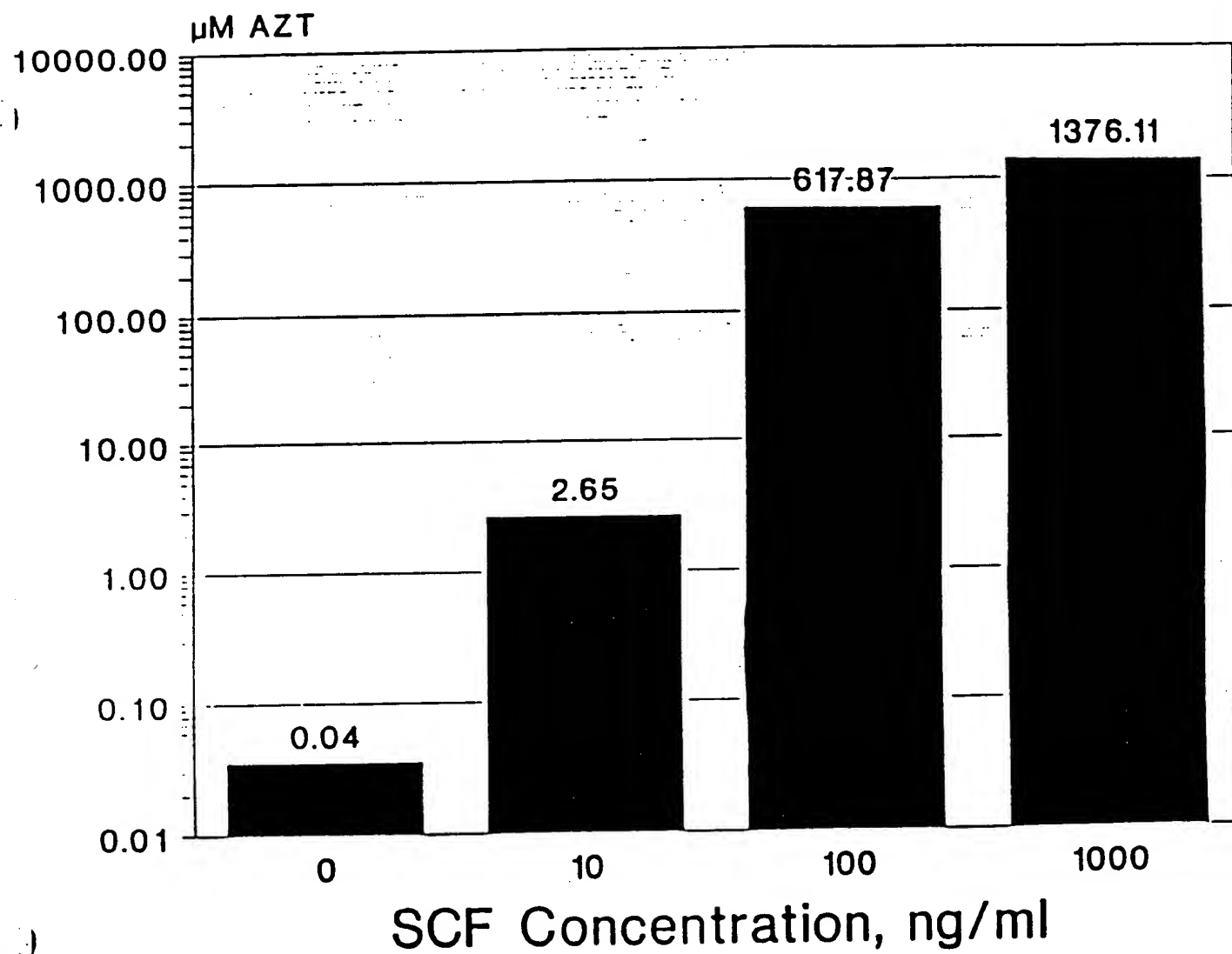


FIG. 62

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

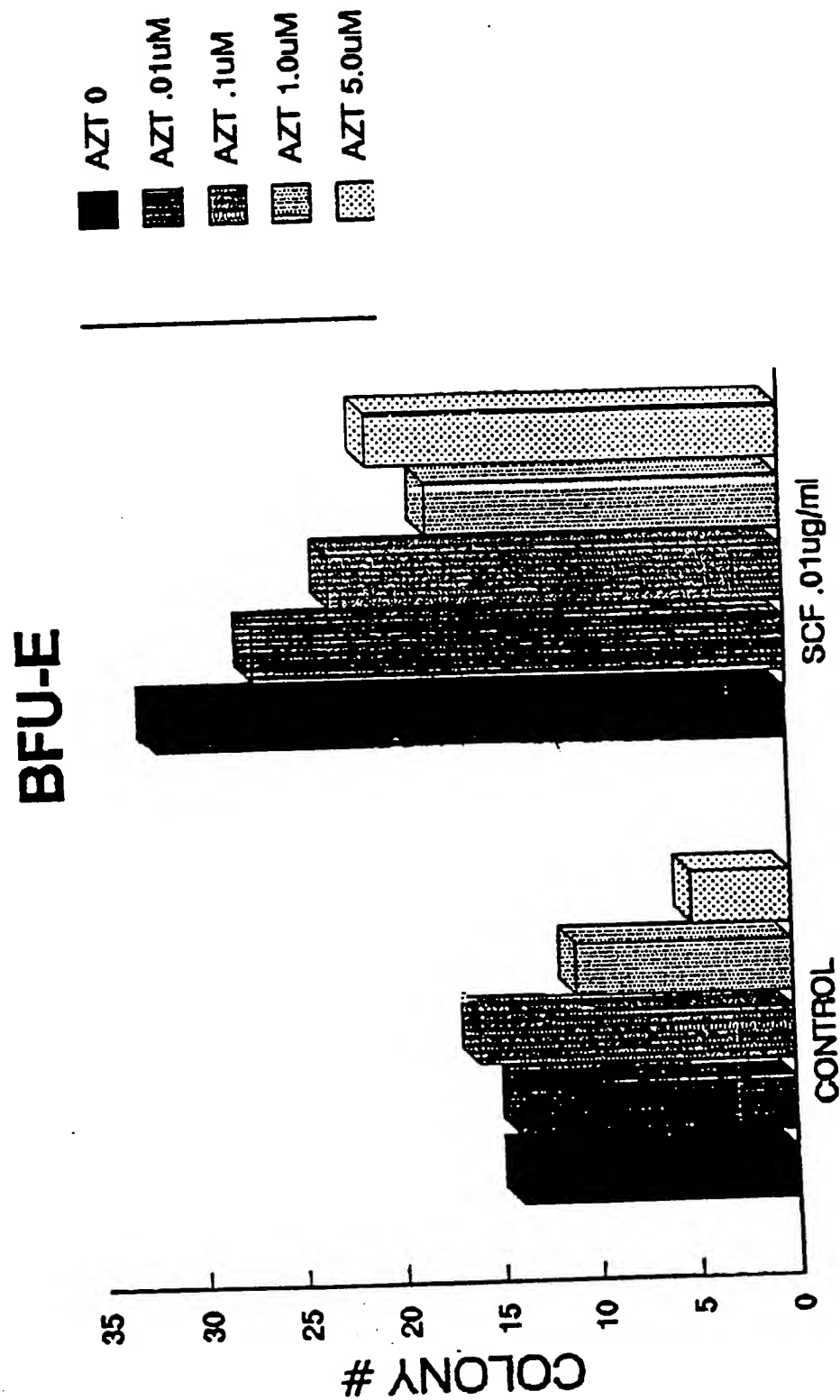


FIG. 63

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

CFU-GM

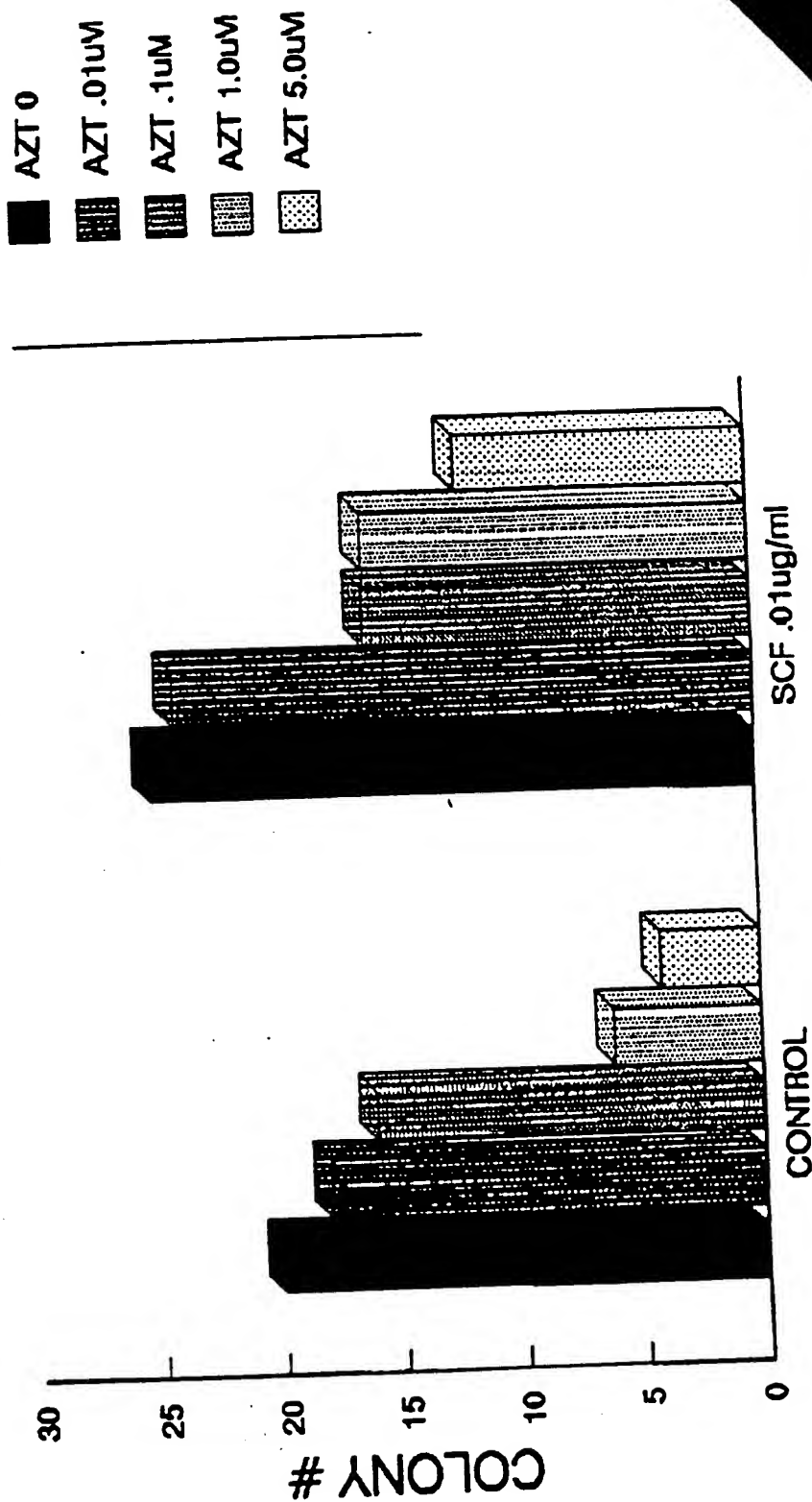


FIG. 64

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

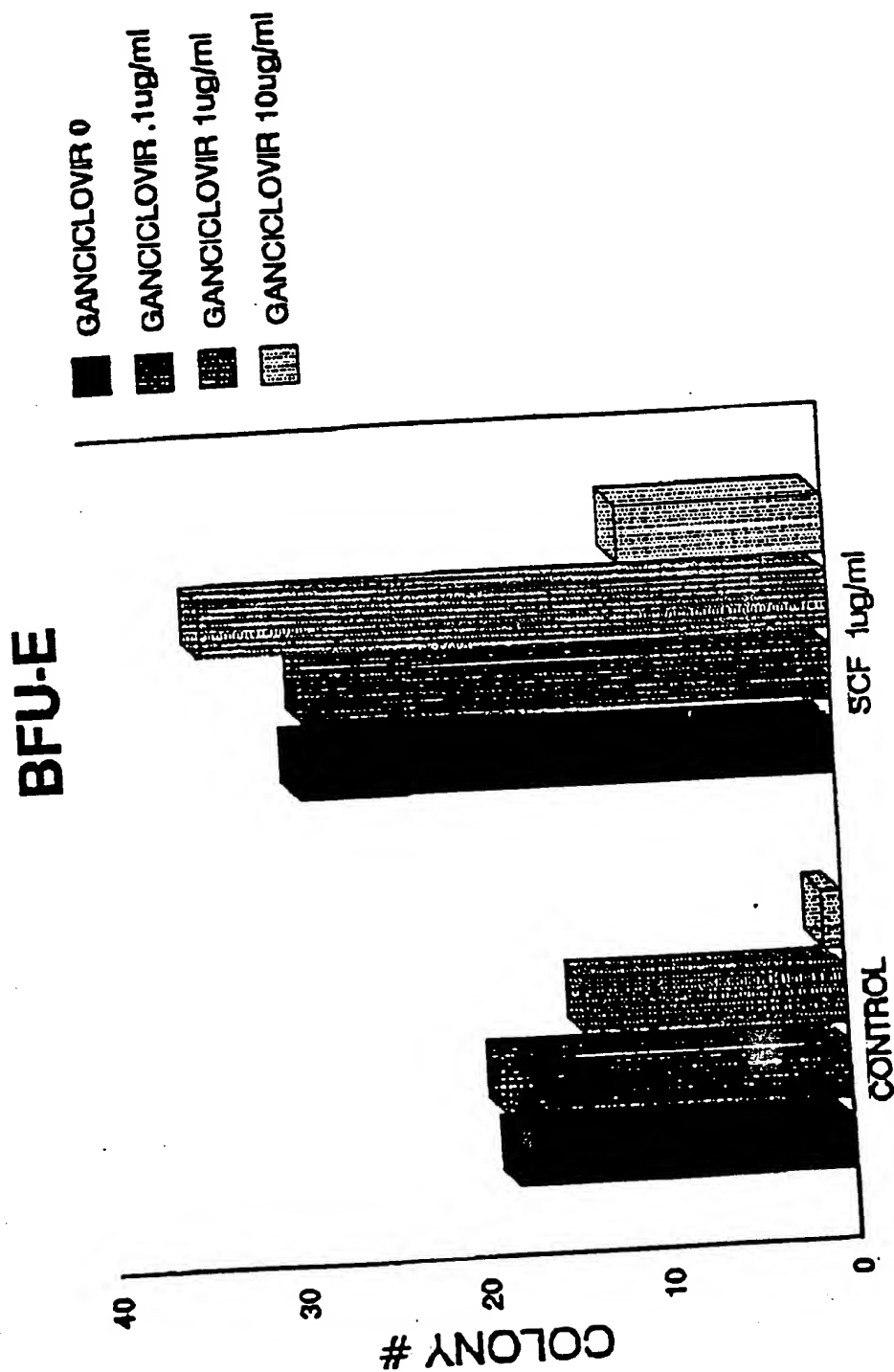


FIG. 65

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

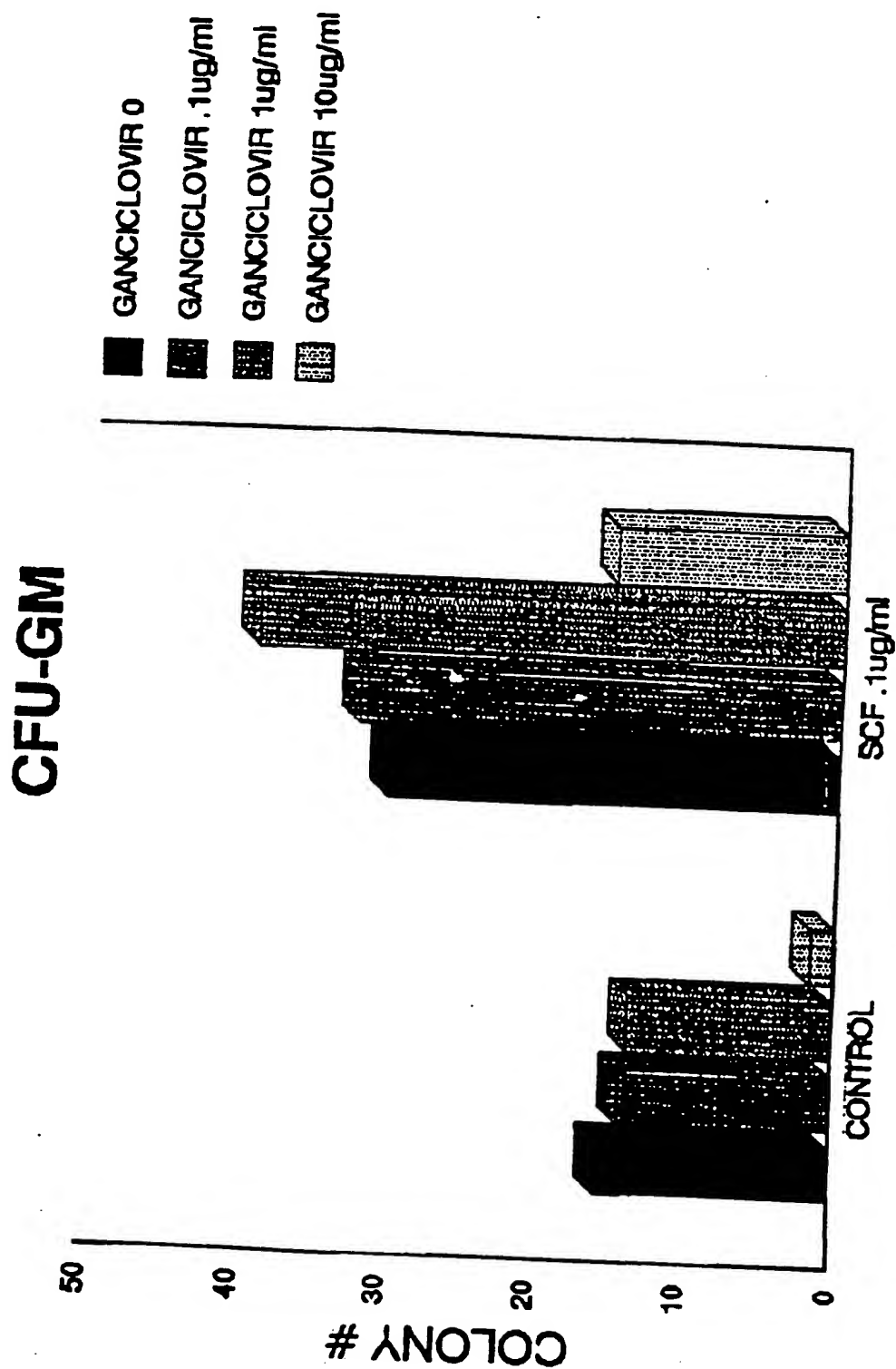


FIG. 66

Effects of SCF on CFU-S Number

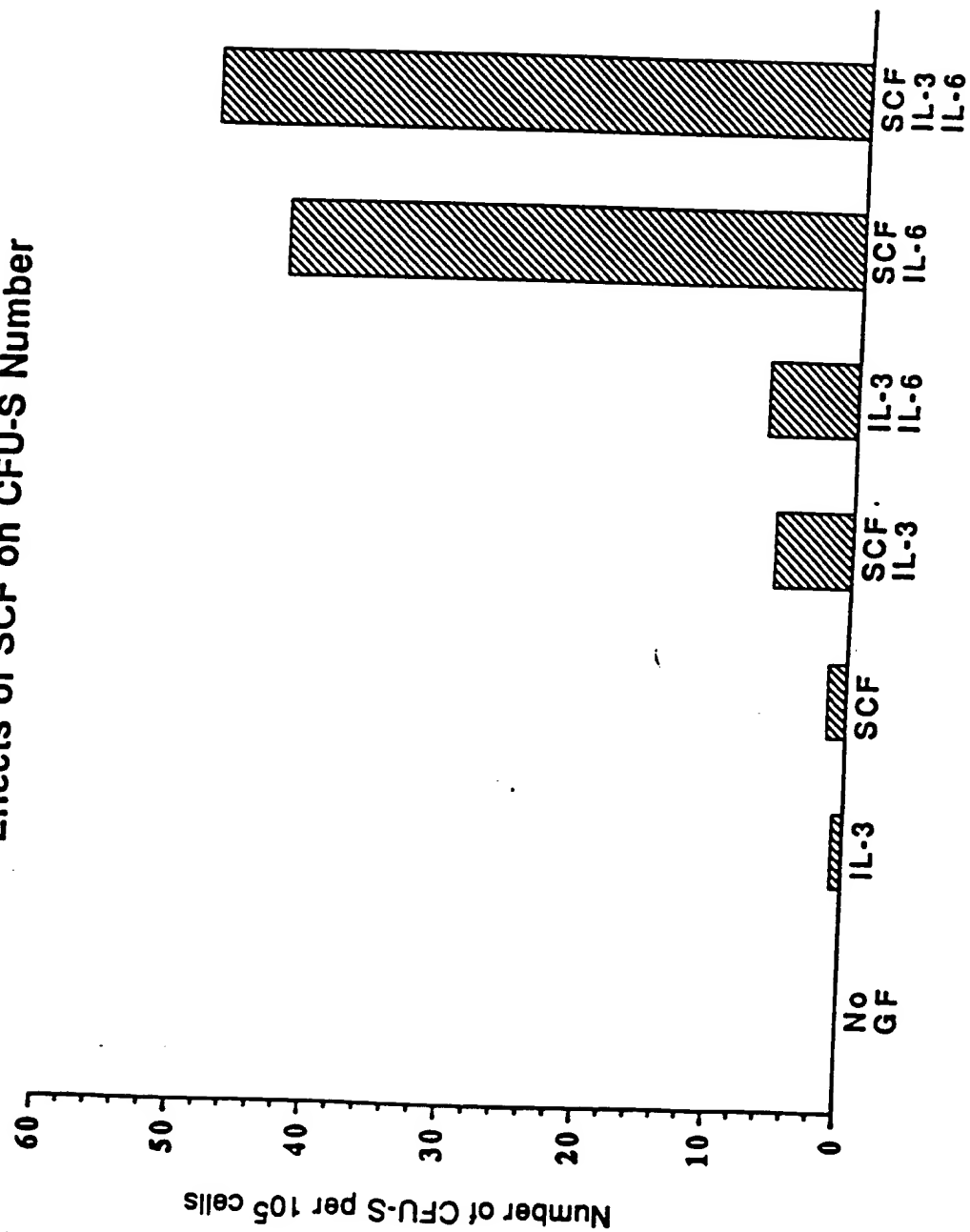


FIG. 67

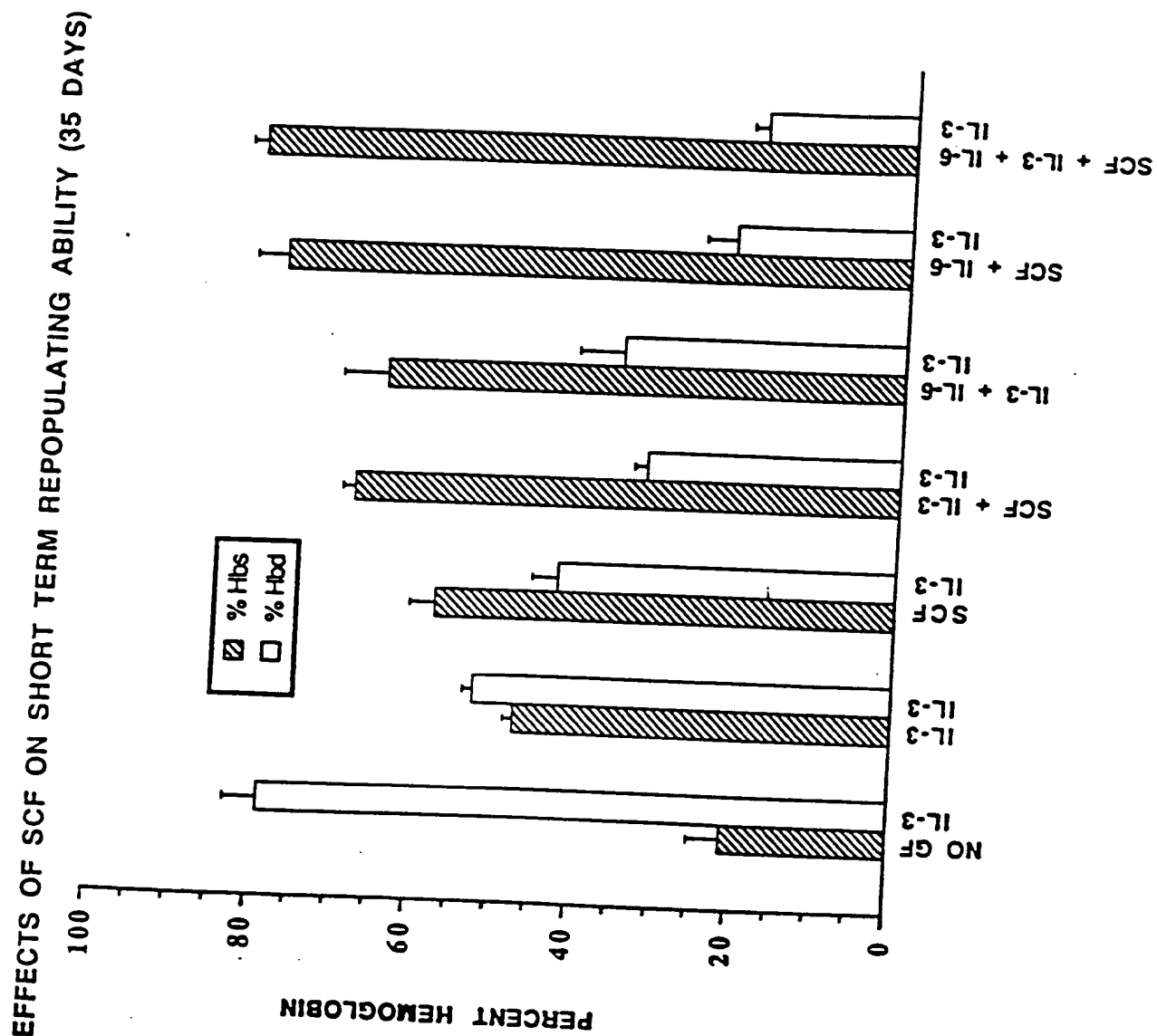


FIG. 68

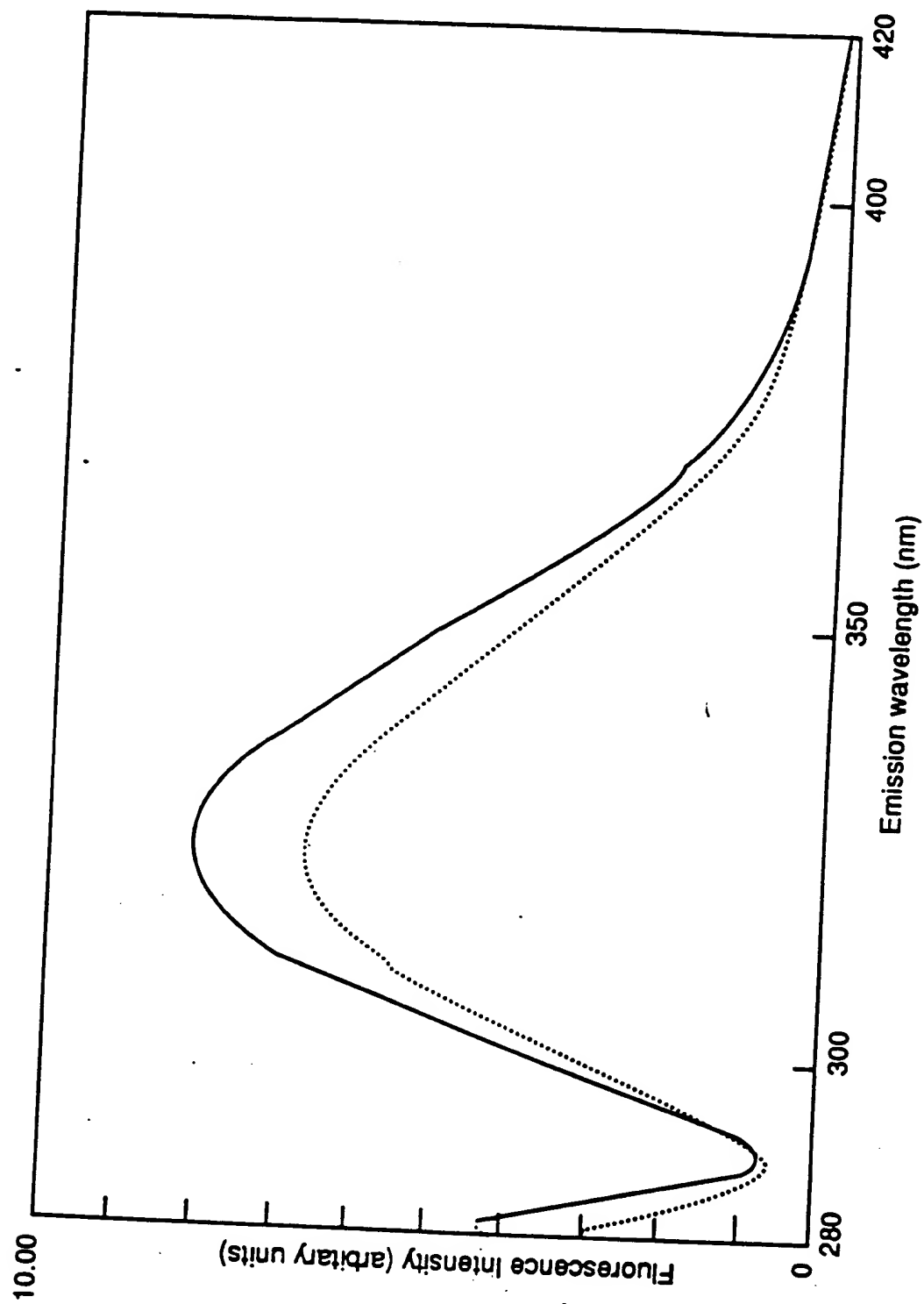


FIG. 69A

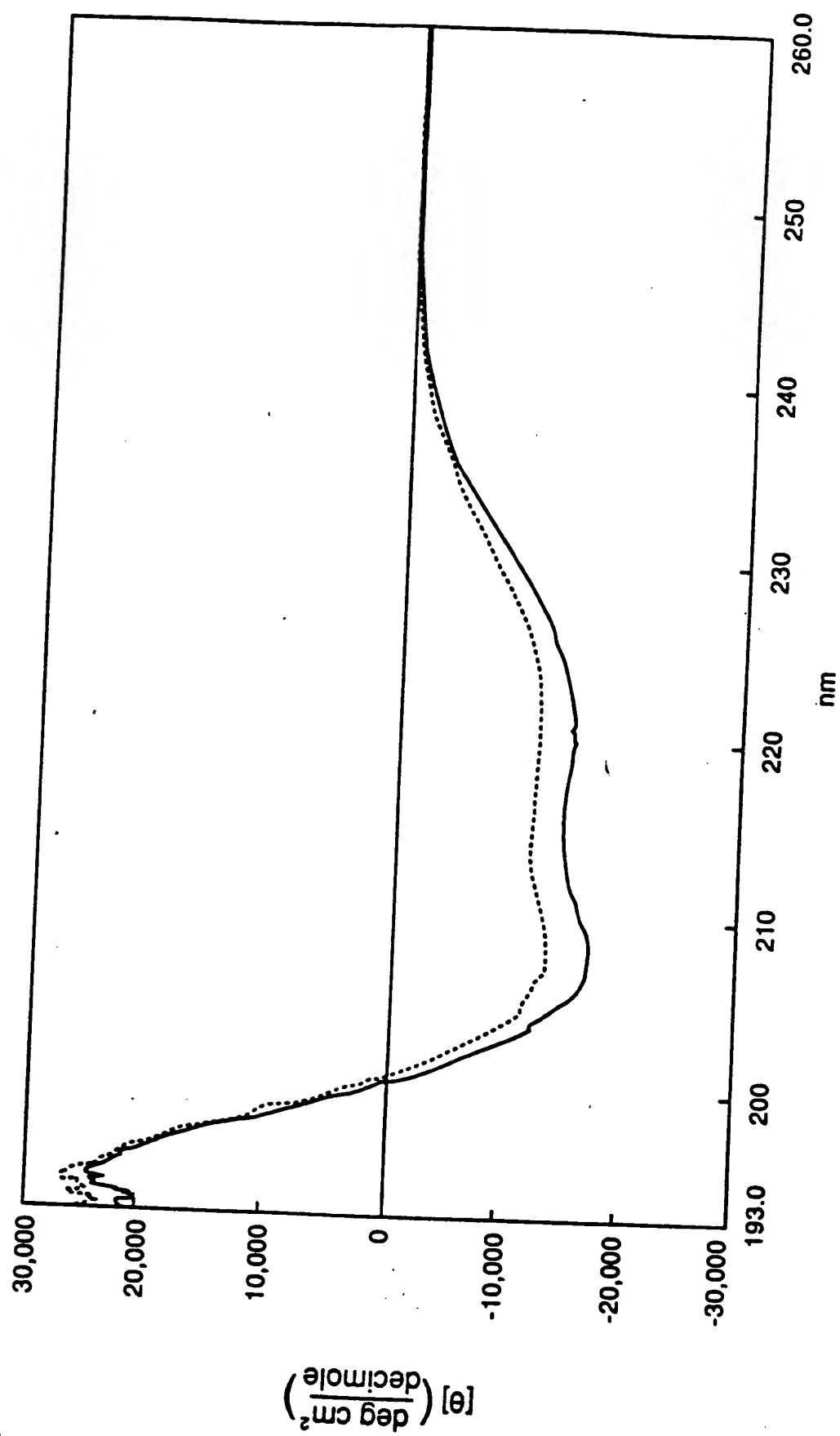


FIG. 69B

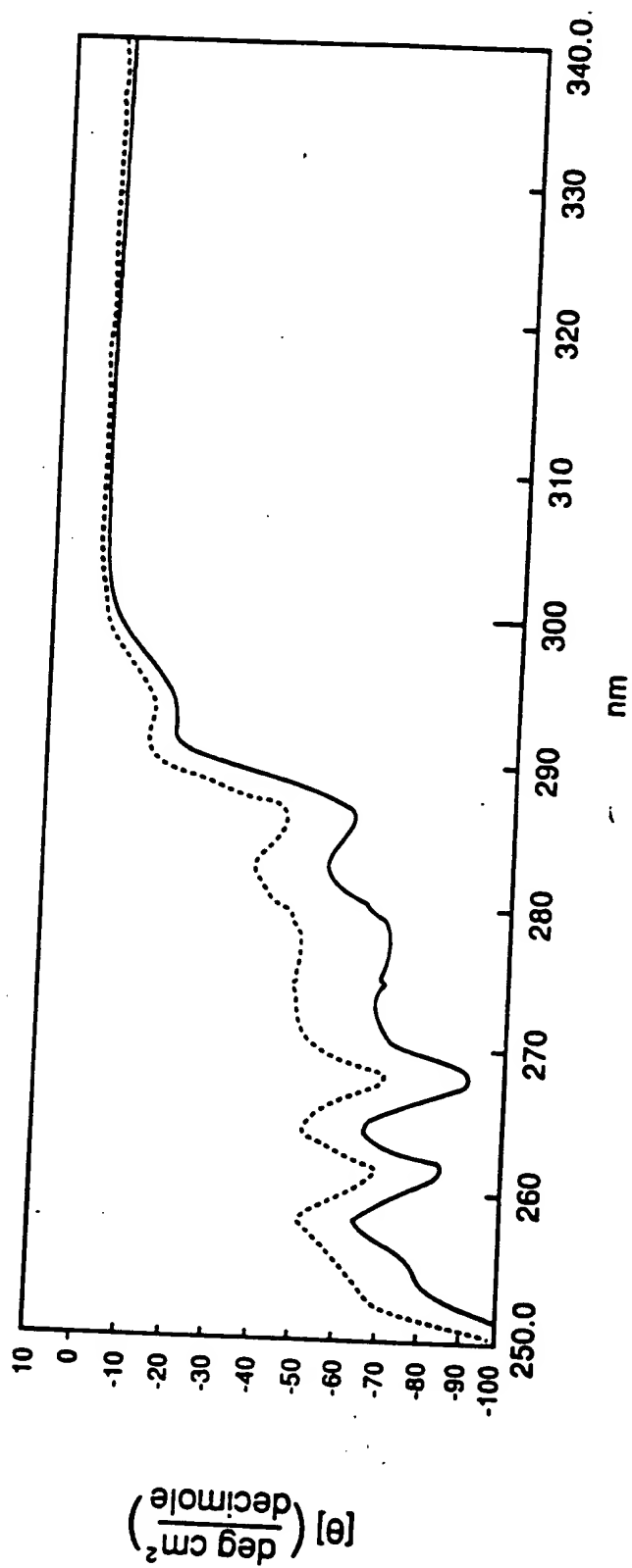


FIG. 70

